; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 1191; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
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Query Match 100.0%; Score 1191; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
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;  PRIOR APPLICATION NUMBER: 60/084441
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;  PRIOR FILING DATE: 1998-5-07
;  PRIOR APPLICATION NUMBER: 60/084627
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;  PRIOR APPLICATION NUMBER: 60/084643
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085339
;  PRIOR FILING DATE: 1998-05-13
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;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085323
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;  PRIOR APPLICATION NUMBER: 60/085582
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;  PRIOR FILING DATE: 1998-05-15
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085573
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

  Query Match             100.0%;  Score 1191;  DB 10;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-123;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 6
US-09-978-608A-162
; Sequence 162, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 162
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-608A-162

  Query Match             100.0%;  Score 1191;  DB 10;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-123;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 7
US-09-978-585A-162
; Sequence 162, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
```

; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-162

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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RESULT 8
US-09-978-191A-162
; Sequence 162, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/084643
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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RESULT 9
US-09-978-403A-162
; Sequence 162, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/078939
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Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
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Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
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; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Botstein, David
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
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; PRIOR APPLICATION NUMBER: 60/084637
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; PRIOR APPLICATION NUMBER: 60/084639
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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RESULT 12
US-09-981-915A-162
; Sequence 162, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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RESULT 13
US-09-978-824-162

; Sequence 162, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db 181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224

RESULT 14
US-09-918-585A-162
; Sequence 162, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 162, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C21
;  CURRENT APPLICATION NUMBER: US/09/978,423A
;  CURRENT FILING DATE:  2002-05-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.9e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

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Search completed: April 7, 2004, 11:59:54
Job time : 44 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 7, 2004, 11:49:59 ; Search time 61 Seconds
(without alignments)
1037.551 Million cell updates/sec

Title: US-10-020-445A-162
Perfect score: 1191
Sequence: 1 MESGAYGAAKAGGSFDLRRF.....QPPFTQNAETTEGYQPPPVY 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1191	100.0	224	2	AAY41709	Aay41709 Human PRO
2	1191	100.0	224	3	AAB44265	Aab44265 Human PRO
3	1191	100.0	224	3	AAB24048	Aab24048 Human PRO
4	1191	100.0	224	4	AAB64539	Aab64539 Gene 45 h
5	1191	100.0	224	6	ABO25211	Abo25211 Novel hum
6	1191	100.0	224	6	ABU72217	Abu72217 Novel hum
7	1191	100.0	224	6	ABU84897	Abu84897 Human sec
8	1191	100.0	224	6	ABU61095	Abu61095 Human PRO
9	1191	100.0	224	6	ABU80364	Abu80364 Human sec
10	1191	100.0	224	6	ADA24701	Ada24701 Novel hum
11	1191	100.0	224	6	ABO19666	Abo19666 Novel hum
12	1191	100.0	224	6	ADA12362	Ada12362 Human sec
13	1191	100.0	224	6	ABO19557	Abo19557 Novel hum
14	1191	100.0	224	7	ADB73668	Adb73668 Human PRO
15	1191	100.0	224	7	ADB76384	Adb76384 Human PRO
16	1191	100.0	224	7	ADC43810	Adc43810 Human sec
17	1191	100.0	224	7	ADC61570	Adc61570 Human sec
18	1191	100.0	224	7	ADC63534	Adc63534 Human sec
19	1191	100.0	224	7	ADC66634	Adc66634 Human sec
20	1191	100.0	224	7	ADC68758	Adc68758 Human sec
21	1191	100.0	224	7	ADC62818	Adc62818 Human sec
22	1191	100.0	224	7	ADC67883	Adc67883 Human sec
23	1191	100.0	224	7	ADC41203	Adc41203 Human sec
24	1191	100.0	224	7	ADC67258	Adc67258 Human sec
25	1191	100.0	224	7	ADC62194	Adc62194 Human sec
26	1191	100.0	224	7	ADC41827	Adc41827 Human sec
27	1191	100.0	224	7	ADD45142	Add45142 Human Pro
28	1191	100.0	224	7	ADE54986	Ade54986 Human Pro
29	1191	100.0	224	7	ADE49196	Ade49196 Human sec
30	1191	100.0	224	7	ADE35250	Ade35250 Human sec
31	1191	100.0	224	7	ADE16364	Ade16364 Human sec
32	1191	100.0	224	7	ADD72979	Add72979 Human sec
33	1191	100.0	224	7	ADD72337	Add72337 Human sec
34	1191	100.0	224	7	ADE16988	Ade16988 Human sec
35	1191	100.0	224	8	ADE48496	Ade48496 Human sec
36	1191	100.0	224	8	ADE89597	Ade89597 Human sec
37	1185	99.5	224	2	AAW36516	Aaw36516 Human syn
38	1184	99.4	224	4	AAB64466	Aab64466 Human sec
39	1184	99.4	224	4	AAB64540	Aab64540 Human sec
40	1184	99.4	240	3	AAB43978	Aab43978 Human can
41	1141.5	95.8	233	4	ABG22771	Abg22771 Novel hum
42	1055	88.6	234	7	ADE54984	Ade54984 Rat Prote
43	1055	88.6	234	7	ADD45140	Add45140 Rat Prote
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45	735	61.7	162	3	AAB51881	Aab51881 Human sec

ALIGNMENTS

RESULT 1
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ID AAY41709 standard; protein; 224 AA.
XX
AC AAY41709;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO615 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34027.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 61; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
```

RESULT 2
AAB44265
ID AAB44265 standard; protein; 224 AA.
XX
AC AAB44265;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO615 (UNQ352) protein sequence SEQ ID NO:162.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78493.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 12; Fig 61; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
```

RESULT 3
AAB24048
ID AAB24048 standard; protein; 224 AA.
XX
AC AAB24048;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO615 protein sequence SEQ ID NO:16.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
KW tumourigenesis; detection; neoplastic cell growth; proliferation;
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
KW immunological disorder.
XX
OS Homo sapiens.
XX

PN WO200053754-A1.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000277.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
PI Wood WI;
XX
DR WPI; 2000-572269/53.
DR N-PSDB; AAC58232.
XX
PT New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment.
XX
PS Claim 61; Fig 16; 195pp; English.
XX
CC The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO538, PRO3664, PRO618,
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions and
CC methods for the diagnosis and treatment of neoplastic cell growth and
CC proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumour cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumour treatment. Compounds
CC that inhibit the expression or activity of the identified polypeptides
CC can be identified and used as antagonists. Benign or malignant tumours,
CC inflammatory disorders and immunological disorders can be treated.
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
```

RESULT 4

```
AAB64539
ID   AAB64539 standard; protein; 224 AA.
XX
AC   AAB64539;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Gene 45 human secreted protein homologous amino acid sequence #177.
XX
KW   Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW   fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
KW   hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW   cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
KW   angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
KW   ocular disorder; corneal infection; wound healing; food additive;
KW   preservative.
XX
OS   Homo sapiens.
XX
PN   WO200077255-A1.
XX
PD   21-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US014926.
XX
PR   11-JUN-1999;   99US-0138628P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis GA;
XX
DR   WPI; 2001-025337/03.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is used
PT   in preventing, treating or ameliorating a medical condition.
XX
PS   Disclosure; Page 582-583; 593pp; English.
XX
CC   The polynucleotide sequences given in AAF32699 to AAF32747 encode the
CC   human secreted proteins given in AAB64422 to AAB64470. AAB64471 to
CC   AAB64548 represent human secreted polypeptide sequences and proteins
CC   homologous to them, which are given in the exemplification of the present
CC   invention. Human secreted proteins have activities based on the tissues
CC   and cells the genes are expressed in. Examples of activities include:
CC   antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC   cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
CC   neuroprotective; antibacterial; virucide; fungicide; and
CC   ophthalmological. The polynucleotides and polypeptides can be used to
CC   prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC   rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC   in diagnosing a pathological condition or susceptibility to a
CC   pathological condition. Disorders which are diagnosed or treated include
CC   autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC   disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC   e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC   angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC   infections caused by bacteria, viruses and fungi and ocular disorders
CC   e.g. corneal infection. The polypeptides can also be used to aid wound
CC   healing and epithelial cell proliferation, to prevent skin aging due to
CC   sunburn, to maintain organs before transplantation, for supporting cell
CC   culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC   polypeptides can also be used as a food additive or preservative to
CC   increase or decrease storage capabilities. AAF32690 to AAF32698 and
CC   AAB64421 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 224 AA;

  Query Match             100.0%;  Score 1191;  DB 4;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-128;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 5
ABO25211
ID   ABO25211 standard; protein; 224 AA.
XX
AC   ABO25211;
XX
DT   09-SEP-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO615.
XX
KW   Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW   cell death; growth induction cascade; blood coagulation cascade;
KW   viral infection.
XX
OS   Homo sapiens.
XX
PN   US2003050239-A1.
XX
PD   13-MAR-2003.
XX
PF   15-OCT-2001; 2001US-00978191.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   31-MAR-1998;   98US-0080105P.
PR   31-MAR-1998;   98US-0080107P.
PR   31-MAR-1998;   98US-0080165P.
PR   31-MAR-1998;   98US-0080194P.
PR   01-APR-1998;   98US-0080327P.
PR   01-APR-1998;   98US-0080328P.
PR   01-APR-1998;   98US-0080333P.
PR   01-APR-1998;   98US-0080334P.
PR   08-APR-1998;   98US-0081049P.
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PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
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PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
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PR 26-JUN-1998; 98US-00105413.
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PR 01-JUL-1998; 98US-0091359P.
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PR 07-DEC-1998; 98US-00202054.
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PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
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PR 29-OCT-1999; 99US-0162506P.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
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PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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RESULT 6
ABU72217
ID ABU72217 standard; protein; 224 AA.
XX
AC ABU72217;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO615.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 08-APR-1998; 98US-0081049P.
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PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
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PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
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PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX

DR WPI; 2003-328860/31.
DR N-PSDB; ACA63595.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 12; Fig 61; 453pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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RESULT 7
ABU84897
ID ABU84897 standard; protein; 224 AA.
XX
AC ABU84897;
XX
DT 12-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane polypeptide PRO615.
XX
KW Human; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
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PR 17-MAR-1998; 98US-00040220.
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PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328499/31.
DR N-PSDB; ACA71759.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
PS Claim 12; SEQ ID NO 162; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preeclampsia; carcinogenesis. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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RESULT 8
ABU61095
ID ABU61095 standard; protein; 224 AA.
XX
AC ABU61095;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO615 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-00978697.
XX
PR 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
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PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.

PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR N-PSDB; ABX92399.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
PS Claim 12; Fig 61; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. ABU61071-ABU61164 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
Db 1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy 121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
Db 121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy 181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
Db 181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224

RESULT 9
ABU80364
ID ABU80364 standard; protein; 224 AA.
XX
AC ABU80364;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO615.
XX
KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
KW inflammatory disease; necrosis; atherosclerosis; infertility;
KW premature aging; psoriasis; inflammatory disease; renal disease;
KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
KW multiple sclerosis; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003004102-A1.
XX
PD 02-JAN-2003.
XX
PF 15-OCT-2001; 2001US-00978189.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-341189/32.
DR N-PSDB; ACA66140.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
PS Claim 12; Fig 61; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO polypeptide
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db 1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

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Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 10
ADA24701
ID   ADA24701 standard; protein; 224 AA.
XX
AC   ADA24701;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO615.
XX
KW   Human; secreted and transmembrane protein; PRO; tissue typing;
KW   chromosome identification; vaccine; cancer; retinal disorder;
KW   sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW   wound healing; obesity; diabetes; hearing loss;
KW   cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW   haemoglobin associated disorder.
XX
OS   Homo sapiens.
XX
PN   US2003050241-A1.
XX
PD   13-MAR-2003.
XX
PF   16-OCT-2001; 2001US-00978564.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   20-MAR-1998;   98US-0078886P.
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PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
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PR   28-MAY-1998;   98US-0087106P.
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PR   26-JUN-1998;   98US-0090863P.
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PR   01-JUL-1998;   98US-0091359P.
PR   30-JUL-1998;   98US-0094651P.
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PR   07-OCT-1998;   98WO-US021141.
PR   20-NOV-1998;   98US-0109304P.
PR   20-NOV-1998;   98WO-US024855.
PR   22-DEC-1998;   98US-0113296P.
PR   23-DEC-1998;   98US-0113621P.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   12-MAR-1999;   99US-0123957P.
PR   29-MAR-1999;   99US-0126773P.
PR   21-APR-1999;   99US-0130232P.
PR   26-APR-1999;   99US-0131022P.
PR   28-APR-1999;   99US-0131445P.
PR   14-MAY-1999;   99US-0134287P.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   16-JUN-1999;   99US-0139557P.
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PR   23-JUN-1999;   99US-0141037P.
PR   07-JUL-1999;   99US-0142680P.
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PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001WO-US009552.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-521814/49.
DR   N-PSDB; ADA24700.
XX
PT   New isolated PRO polypeptides for example extracellular, secreted and
PT   membrane bound proteins, useful for modulating the biological activities
PT   of cells and for treating, for example diabetes, cancer, rheumatoid
PT   arthritis, and hearing loss.
XX
PS   Claim 12; Fig 61; 461pp; English.
XX
CC   The invention describes an isolated secreted and transmembrane (PRO)
CC   polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC   polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC   useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC   useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC   useful for linking a bioactive molecule to a cell expressing a PRO337
CC   polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC   cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC   bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

  Query Match           100.0%;  Score 1191;  DB 6;  Length 224;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-128;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 11
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ID   ABO19666 standard; protein; 224 AA.
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AC   ABO19666;
XX
DT   08-SEP-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO615.
XX
KW   Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW   peripheral neuropathy; diabetic peripheral neuropathy;
KW   AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW   Refusum's disease; Abetalipoproteinaemia; Tangier disease;
KW   Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW   Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003050240-A1.
XX
PD   13-MAR-2003.
XX
PF   16-OCT-2001; 2001US-00978403.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
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PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
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PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
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PR   30-MAR-1998;   98US-0079923P.
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PR   31-MAR-1998;   98US-0080107P.
PR   31-MAR-1998;   98US-0080165P.
PR   31-MAR-1998;   98US-0080194P.
PR   01-APR-1998;   98US-0080327P.
PR   01-APR-1998;   98US-0080328P.
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PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
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PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
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PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
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PR 02-JUN-1999; 99WO-US012252.
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PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
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PR 30-NOV-1999; 99WO-US028313.
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PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
DR WPI; 2003-503575/47.
DR N-PSDB; ACD29741.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 61; 459pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,
CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's

Query Match 100.0%; Score 1191; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;

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  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60
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Db          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCV 60

Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Db         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120

Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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Db        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180

Qy        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224
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Db        181 YVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY 224


RESULT 12
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ID   ADA12362 standard; protein; 224 AA.
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AC   ADA12362;
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DT   06-NOV-2003  (first entry)
XX
DE   Human secreted/transmembrane polypeptide PRO615.
XX
KW   inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW   infertility; birth defect; premature aging; AIDS; cancer;
KW   diabetic complication; tissue typing; human.
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OS   Homo sapiens.
XX
PN   US2003055216-A1.
XX
PD   20-MAR-2003.
XX
PF   17-OCT-2001; 2001US-00978824.
XX
PR   21-MAY-1996;   96US-0018049P.
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
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PR   20-MAR-1998;   98US-0078886P.
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PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
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PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   31-MAR-1998;   98US-0080105P.
PR   31-MAR-1998;   98US-0080107P.
PR   31-MAR-1998;   98US-0080165P.
PR   31-MAR-1998;   98US-0080194P.
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PR   21-APR-1998;   98US-0082569P.
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PR 22-DEC-1998; 98US-0113296P.
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PR 28-JUL-1999; 99US-0146222P.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
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PR 06-JAN-2000; 2000WO-US000277.
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PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Perrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

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RESULT 13
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AC ABO19557;
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DT 27-AUG-2003 (first entry)
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KW Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosum; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinaemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac- insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978585.
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PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
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DT   04-DEC-2003  (first entry)
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DE   Human PRO polypeptide #25.
XX
KW   Human; PRO polypeptide; secreted protein; transmembrane protein;
KW   cell death; neuropathy; neuropathy related disease;
KW   Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW   chromosome mapping; gene mapping; genetic disorder; septic shock;
KW   antibacterial; immunosuppressive; neuroprotective.
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OS   Homo sapiens.
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PN   US2003045462-A1.
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PD   06-MAR-2003.
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PF   16-OCT-2001; 2001US-00978608.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX

Query Match 100.0%; Score 1191; DB 7; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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ID ADB76384 standard; protein; 224 AA.
XX
AC ADB76384;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #25.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective.
XX
OS Homo sapiens.
XX
PN US2003083248-A1.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2001; 2001US-00978757.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-755118/71.
DR N-PSDB; ADB76383.
XX
PT New PRO polypeptides useful for treating peripheral neuropathy,

PT neuropathies associated with systemic disease such as post-polio syndrome
PT or AIDS-associated syndrome.
XX
PS Claim 12; Fig 61; 425pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides
CC are useful for treating neuropathy and neuropathy related diseases such
CC as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation

Query Match 100.0%; Score 1191; DB 7; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Job time : 63 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
12302.893 Million cell updates/sec

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Perfect score: 1512
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	22	894.6	59.2	1201	13	BX377649	BX377649 BX377649
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	46	816.4	54.0	861	13	BU542737	BU542737 AGENCOURT
	47	814.2	53.8	910	13	BU541667	BU541667 AGENCOURT
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	50	809.4	53.5	882	13	BU539619	BU539619 AGENCOURT
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	66	784.4	51.9	925	13	BQ643190	BQ643190 AGENCOURT
	67	783.2	51.8	939	13	BU844978	BU844978 AGENCOURT
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	71	778.8	51.5	1063	12	BM924627	BM924627 AGENCOURT
	72	774.6	51.2	803	12	BI669811	BI669811 603293394
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	86	756.8	50.1	920	13	BQ952448	BQ952448 AGENCOURT
	87	756	50.0	868	14	CA489434	CA489434 AGENCOURT
	88	756	50.0	1046	12	BG164178	BG164178 602343065
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	90	755.6	50.0	921	13	BQ892654	BQ892654 AGENCOURT
	91	755.6	50.0	1086	12	BM423602	BM423602 AGENCOURT
	92	755.4	50.0	936	13	BQ225128	BQ225128 AGENCOURT
c	93	754.8	49.9	901	13	BX372675	BX372675 BX372675
c	94	754.2	49.9	790	14	CB243767	CB243767 UI-CF-FN0
c	95	753.6	49.8	897	12	BI490863	BI490863 603031836
	96	752.8	49.8	874	13	BQ898257	BQ898257 AGENCOURT
	97	752.8	49.8	948	14	CA487641	CA487641 AGENCOURT
	98	750	49.6	770	12	BG685353	BG685353 602637791
c	99	749.8	49.6	779	13	BU621107	BU621107 UI-H-FL1-
	100	749.2	49.6	836	12	BI597268	BI597268 603250553

ALIGNMENTS

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RESULT 1
AL578846/c
LOCUS       AL578846                1145 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  AL578846 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK006YH24 3-PRIME, mRNA sequence.
ACCESSION   AL578846
VERSION     AL578846.2  GI:31317034
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1145)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12943315.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK006DD12NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK006DD12NP1.
FEATURES             Location/Qualifiers
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                     /clone="CS0DK006YH24"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             66.2%;  Score 1000.4;  DB 9;  Length 1145;
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  Best Local Similarity   95.6%;  Pred. No. 1.1e-168;
  Matches 1077;  Conservative   14;  Mismatches   26;  Indels   10;  Gaps    6;

Qy        378 CTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAG 437
              |:  |||     :| | ||||||||||| ||: : : |:|    :|||||||:|:||||
Db       1122 CYGCTCTTTCAGYTTTTGACCTTCCTGTGTTTKTKGKTTYT---GYTCCTCACMAMCCAG 1066

Qy        438 TGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATC 497
              | |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1065 T-GGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGCCCGACTCTGTGAGGGCAGCCATC 1007

Qy        498 ACCTTCAGCTTC-TTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCG 556
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 ACCTTCAGCTTCTTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCG 947

Qy        557 CTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAA 616
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        946 CTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACG-TGACCCCACTCCGGACCCCAA 888

Qy        617 CACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCAC 676
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Db        887 CACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCAC 828

Qy        677 CCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAG 736
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        827 CCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAG 768

Qy        737 CGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCT 796
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        767 CGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCT 708

Qy        797 GGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGG 856
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Db        707 GGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGG 648

Qy        857 AGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGC 916
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 AGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGC 588

Qy        917 TTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTT 976
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 TTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTT 528

Qy        977 TCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATG 1036
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Db        527 TCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATG 468

Qy       1037 TGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATT 1096
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Db        467 TGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATT 408

Qy       1097 ATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCC 1156
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Db        407 ATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCC 348

Qy       1157 GGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATC 1216
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Db        347 AGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATC 288

Qy       1217 TGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGG 1276
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Db        287 TGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGG 228

Qy       1277 CTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCT 1336
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Db        227 CTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCT 168

Qy       1337 GACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGC 1396
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Db        167 GACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGC 108

Qy       1397 AGGGGTGCCCCATGGCTCCCAGA-CTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGG 1455
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Db        107 AGGGGTGCCCCATGGCTCCCMSACCTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGG 48

Qy       1456 GAGATGCCCGG---CCTGGGATGCTGTTTGGAGACGGAATAAATGTT 1499
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Db         47 GAGATGNCCCGGNCCTGGGNATGCTGTTBNMHGYCGVAATAAATGTT 1
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RESULT 2
AL556634

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LOCUS       AL556634               1131 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL556634 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK006YH24 5-PRIME, mRNA sequence.
ACCESSION   AL556634
VERSION     AL556634.2  GI:31278435
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1131)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12899489.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK006DD12QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK006DD12QP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK006YH24"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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Query Match 64.0%; Score 968.2; DB 9; Length 1131;
Best Local Similarity 97.1%; Pred. No. 6.4e-163;
Matches 1042; Conservative 6; Mismatches 19; Indels 6; Gaps 6;

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Qy          53 GGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 112
               ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          64 GGGATGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 123

Qy         113 GACGCAGCCGCAGGTGG-TGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCT 171
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db         124 GACGCAGCCGCAGGTGGNTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCT 183

Qy         172 CCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGT 231
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 CCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGT 243

Qy         232 TCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGG 291
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Db         244 TCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGG 303

Qy         292 CCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACC 351
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Db         304 CCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACC 363

Qy         352 GCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTG 411
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Db         364 GCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTG 423

Qy         412 TTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGG 471
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Db         424 TTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGG 482

Qy         472 GGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTG 531
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Qy         532 TGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATT 591
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Qy         592 ACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGG 651
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Qy         772 CCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATC 831
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Db         783 CCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATC 842

Qy         832 CTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACA 891
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Db         843 CTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACA 901

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Db         902 CCCCAAGTGCCTGTGCCCAGAGGGTTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTA 961

Qy         952 GGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGT 1011
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Db         962 GGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAG-CCCGCCTGCAGT 1020

Qy        1012 GGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCC 1071
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Db        1021 GGCTAGAAGCCAGCAGGTGGCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCSGG-CC 1079

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RESULT 3
AL563019/c

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LOCUS       AL563019               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL563019 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC027YP17 3-PRIME, mRNA sequence.
ACCESSION   AL563019
VERSION     AL563019.2  GI:31287026
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12912018.
            Contact: Genoscope
```

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8916.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC027CH09NP1&cluster=8916.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC027CH09NP1.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 63.6%; Score 962.2; DB 9; Length 1201;
Best Local Similarity 95.4%; Pred. No. 7.7e-162;
Matches 1037; Conservative 14; Mismatches 29; Indels 7; Gaps 6;

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Qy        399 TTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAG 458
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Db       1098 TKGCCCTYCTTTGTTTKTTGTTTYGCTCCTCMCAACCAGT-GGAAATMACCAACCCAAAG 1040

Qy        459 GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATC 518
              :|||:|||||||||| || |:|:|||||||||:|||||||||||||||||||||||||||
Db       1039 RACGYGCTGGTGGGGCCC-AMTYTGTGAGGGCASCCATCACCTTCAGCTTCTTTTCCATC 981

Qy        519 TTCTCCTGGGGTGTGCTGGCC-TCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGA 577
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Db        980 TTCTCCTGGGGTGCGCTGGCCTTCCCTGGCCTACCAGCGCAACAAGGCTGGCGTGGACGA 921

Qy        578 CTTCATCCAGAATTACGTTGACCCCACTCCGGA-CCCCAACACTGCCTACGCCTCCTACC 636
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Db        920 CTTCATCCAGAATTACGTTGACCCCACTCCGGAMCCCCAACACTGCCTACGCCTCCTACC 861

Qy        637 CAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG 696
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Db        800 AGGGCTACCAGCCGCCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAG 741

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Db        740 AGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGRACTGCCAGCCCCTCTC 681

Qy        816 TTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGG 875
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Db        680 TTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGG 621

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Qy        936 CTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCT 995
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Db        560 CTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTCCCTCGCTTTTAATGACCT 501

Qy        996 CAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTC 1055
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Db        500 CAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCNACTGACAAGTGCCTC 441
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Qy       1056 AGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAA 1115
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Qy       1116 GACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCC 1175
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Db        380 GACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCC 321

Qy       1176 TCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTG 1235
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Db        320 TCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTG 261

Qy       1236 CCGGTGGCCTCTGGGCTGCCT--CCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACT 1293
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Qy       1354 TGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCT 1413
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Db        140 TGTAAATATTCTGCAGTTGTAACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCT 81

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Qy       1474 TGCTGTT 1480
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Db          20 TGCTGTT 14
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RESULT 4
AL546691
LOCUS AL546691 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL546691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029YE05 5-PRIME, mRNA sequence.
ACCESSION AL546691
VERSION AL546691.2 GI:31268524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12880049.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8916.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029AC03QP1&cluster=8916.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029AC03QP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YE05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 63.4%; Score 958.2; DB 9; Length 1201;
Best Local Similarity 94.0%; Pred. No. 4e-161;
Matches 1029; Conservative 18; Mismatches 41; Indels 7; Gaps 5;

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Qy      12 GCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGC 71
           || | |  ||   |   ||| |    |||   |||||||||||||||||||||||||||
Db      28 GCAGGCTGGTACCGGTCCGGAATTCCCGGGATCGGCGACATGGAGAGCGGGGCCTACGGC 87

Qy      72 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 147

Qy     132 GCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 GCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 207

Qy     192 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 267

Qy     252 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTG 311
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Db     268 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTG 327

Qy     312 GTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGT 371
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Db     328 GTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGT 387

Qy     372 GACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACC 431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 GACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACC 447

Qy     432 AACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCA 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 AACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCA 507

Qy     492 GCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTAC 551
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Db     508 GCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTAC 567

Qy     552 CAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGAC 611
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Db     568 CAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGAC 627

Qy     612 CCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCC 671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 CCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCC 687

Qy     672 TTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCG 731
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 TTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCG 747

Qy     732 GTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGC 791
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 GTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGC 807

Qy     792 CTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGC 851
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 CTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGC 867

Qy     852 TAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAG 911
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 TAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCTGTGCCCAG 926

Qy     912 AGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGT 971
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Db     927 AGGSTTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGT 986

Qy     972 GTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGC 1031
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Db     987 GTTTTTCCYCGCTTTTAATGACYYCAG-CCCSCCTGCAGTGGCTARAAG-CARCAGGTGC 1044

Qy    1032 CCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCG 1091
           |    ||: :     ||||||:|||:||  :||||||||||||: || | :||||:  :
Db    1045 CATGTTGYAM--TGAAAGTGCYTCASCT--YCCCCGGCCCGGGYAAGCCGKTGGGRCGST 1100

Qy    1092 CTATTATCTGCGTTC 1106
           |:|| : |   |||
Db    1101 WTWTTTKGTTTTTTC 1115


RESULT 5
AL530639/c
LOCUS       AL530639                1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL530639 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD008YH06 3-PRIME, mRNA sequence.
ACCESSION   AL530639
VERSION     AL530639.2  GI:31068472
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12794132.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            8916.f For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DD008DD03NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DD008DD03NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DD008YH06"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 63.3%; Score 956.4; DB 9; Length 1201;
Best Local Similarity 91.3%; Pred. No. 8.4e-161;
Matches 982; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

Qy     401 CCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGA 460
           ||| |  |:| ||   :| |  :|||   :|||||: : || | |||||||||| |||||
Db    1075 CCTCTTTTKTTTTTTGKTTTCTYTCCCTCMCAACCMAKTGGAATTCACCAACCCAAAGGA 1016

Qy     461 CGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTT 520
           || |:|||||||| || |:|:|:| ||||||:|| ||:|||||||||:|||:||:||||
Db    1015 CGGGBTGGTGGGGCCCAAYTYTKTAAGGGCASCCTTCMCCTTCAGCTTYTTTYCCWTCTT 956

Qy     521 CTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTT 580
           |::|| |||| | | |||  || ||| : |   :  | :| | |:| ||| || ||||
Db     955 CYYCTTGGGTTGGGTTGCCCTCCYTGCCCWACCAGSGCAAMAAGGTKGGGTGAACAACTT 896

Qy     581 CATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGG 640
           :|||:| |||:|||||:||||:|||||||||||||| ||||||||||||||||||||||
Db     895 MATCMAAAATWACGTTRACCCMACTCCGGACCCCAAAACTGCCTACGCCTCCTACCCAGG 836
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Qy       641 TGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGG 700
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Qy       701 CTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGC 760
Db       775 CTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGAACAGAGAGGGC 716

Qy       761 CCTCCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCA 820
Db       715 CCTCCCCCTCTGCCCTGRACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCA 656

Qy       821 CCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTG 880
Db       655 CCTGTTCCATCCTGTGCAGCTAACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCT- 597

Qy       881 GCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCA 940
Db       596 GCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCGGCTMACTCCTCCA 537

Qy       941 GGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCC 1000
Db       536 GGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCC 477

Qy      1001 CCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTT 1060
Db       476 CCGCCTGMAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCAACTRACAAGTGCCTCAGCTT 417

Qy      1061 CCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTC 1120
Db       416 CCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAAACTC 357

Qy      1121 GTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACT 1180
Db       356 GTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTAACT 297

Qy      1181 CAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT 1240
Db       296 CAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT 237

Qy      1241 GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCT 1300
Db       236 GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCT 177

Qy      1301 TGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAAT 1360
Db       176 AGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAAT 117

Qy      1361 ATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGAC 1420
Db       116 ATTCTGCAGTTGTAACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGAC 57

Qy      1421 TCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGC 1476
Db         56 TCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGRATGV 1
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RESULT 6
AL573537/c
LOCUS       AL573537               1185 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL573537 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI049YJ18 3-PRIME, mRNA sequence.
ACCESSION   AL573537
VERSION     AL573537.2  GI:31294882
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1185)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12932878.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI049DE09NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI049DE09NP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI049YJ18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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  Query Match             63.2%;  Score 956;  DB 9;  Length 1185;
  Best Local Similarity   92.3%;  Pred. No. 9.9e-161;
  Matches 1042;  Conservative   41;  Mismatches   38;  Indels    8;  Gaps    8;

Qy        378 CTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAG 437
Db       1129 CYKCTTTCWCASTTTYKCGMCCTYCTGTGRKTTGTTGKTTYCTGTGTCTTAMCAACCCAG 1070

Qy        438 TGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATC 497
Db       1069 T-GRSAGTCACCAACCCGAAGGACKKGYTGKTGGGGCCSWATTYT-TKARGGCAGCCATC 1012

Qy        498 ACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTA-CCAGCG 556
Db       1011 ACYTTCAGCTTYTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTAMCCAGCG 952

Qy        557 CTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC-CCACTCCGGACCCCA 615
Db        951 CTACAAGGTTGGCGTGGACGACTTCATCCAGAATTACGTTGACCTCWAYTCSGGACCCCA 892

Qy        616 ACACTGCCTACGCCTCCTA-CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTC 674
Db        891 AMACTGCCTACGCCTCCTACCCCAGGKGCATCTGTGGACAACTACCAACAGCCACCCTTC 832

Qy        675 ACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTT 734
Db        831 ACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTT 772

Qy        735 AGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTC 794
Db        771 AGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTC 712

Qy        795 CTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAA 854
Db        711 CTGGAACTGCCAGCCCCTCTCTBTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAA 652

Qy        855 GGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGG 914
Db        651 GGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGG 592

Qy        915 GCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTT 974
Db        591 GCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTT 532

Qy        975 TTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCA 1034
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Db        531 TTACCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCA 472

Qy       1035 TGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTA 1094

Db        471 TGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTA 412

Qy       1095 TTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAG 1154

Db        411 TTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAG 352

Qy       1155 CCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGA 1214

Db        351 CCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGMTRTATRA 292

Qy       1215 T-CTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCG 1273

Db        291 TACTGGGRRCCACCACCCTGTGCCGGTGGCCTCTGGGCTRCCTCCCRTGGTGTGAGGGCG 232

Qy       1274 GGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTG 1333

Db        231 GGGCTGGTGCTCATGGCACTTCCTCCTGGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTG 172

Qy       1334 CCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAG 1393

Db        171 CCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTAACTTAGGAAGCCTGGGGAG 112

Qy       1394 GGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGG 1453

Db        111 GGCA-GGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCRARTRTATTATAAAATCGTGG 53

Qy       1454 GGGAGATGCCCGG-CCTGGGATGCTGTTTGGAGACGGAATAAATGTTTT 1501

Db         52 GGGAGATGCCCGGNCCTGAGATTCTTTTTTTATACKNWTTATTTTTTY 4


RESULT 7
AL547324
LOCUS       AL547324               1076 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL547324 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI007YM24 5-PRIME, mRNA sequence.
ACCESSION   AL547324
VERSION     AL547324.2  GI:31269155
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1076)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12881297.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI007BG12QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI007BG12QP1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DI007YM24"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           62.6%;  Score 947;  DB 9;  Length 1076;
  Best Local Similarity  98.8%;  Pred. No. 3.9e-159;
  Matches 1005;  Conservative    1;  Mismatches    6;  Indels    5;  Gaps    5;

Qy         53 GGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 112

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Qy        113 GACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTC 172

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Qy        173 CTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTT 232

Db        183 CTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTT 242

Qy        233 CAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGC 292

Db        243 CAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGC 302

Qy        293 CTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCG 352

Db        303 CTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCG 362

Qy        353 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 412

Db        363 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 422

Qy        413 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGG 472

Db        423 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGGG 481

Qy        473 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 532

Db        482 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 541

Qy        533 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 592

Db        542 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 601

Qy        593 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 652

Db        602 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 661

Qy        653 CAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCC 712

Db        662 CAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCC 721

Qy        713 CCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 772

Db        722 CCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 781

Qy        773 CCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 832

Db        782 CCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 841

Qy        833 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACAC 892

Db        842 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACAC 900

Qy        893 CCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAG 952

Db        901 CCCAAGTGCCTGTGCCCAGA-GGSTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAG 959

Qy        953 GAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTG 1012

Db        960 GAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTG 1019
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Qy       1013 GCTAG-AAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGG 1068
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1020 GCTAGAAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCGGG 1076


RESULT 8
AL530640
LOCUS       AL530640               1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL530640 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD008YH06 5-PRIME, mRNA sequence.
ACCESSION   AL530640
VERSION     AL530640.2  GI:31068473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12794133.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            8916.f For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DD008DD03QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DD008DD03QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DD008YH06"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             62.5%;  Score 945.6;  DB 9;  Length 1201;
  Best Local Similarity   93.6%;  Pred. No. 7.2e-159;
  Matches 1013;  Conservative   31;  Mismatches   32;  Indels    6;  Gaps    6;

Qy         35 CGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTT 94
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 SGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTT 122

Qy         95 CGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTT 154
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        123 CGACCTGCGGCGCTTCCTGACGCAGCCGCA-GTGGTGGCGCGCGCCGTGTGCTTGGTCTT 181

Qy        155 CGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAA 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAA 241

Qy        215 GCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGG 274
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        242 GCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTKCCATCGG 301

Qy        275 GGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGAT 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGAT 361

Qy        335 CAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTG 394
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CAGCAACGCCACTTACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTG 421

Qy        395 GACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCC 481

Qy        455 GAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTC 514
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTC 540

Qy        515 CATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGA 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGA 600

Qy        575 CGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA 660

Qy        635 CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCAC 694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCAC 720

Qy        695 CGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGA 754
              |||||||||||||||||||||||||:||||| ||||||||||||||||||||||||||||
Db        721 CGAGGGCTACCAGCCGCCCCCTGTGTWCTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGA 780

Qy        755 GAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCT 814
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCT 840

Qy        815 CTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGG 874
              |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db        841 CTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCAWAGCCTGGCGG 900

Qy        875 GGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACT 934
              |||:|||:|||| |||| |||||||||||| |||||||| ||||||:|:|:|||||||||
Db        901 GGGSTGGSAGAG-CACAACCCAAGTGCCTGTTCCCAGAGGGTTTCAGTYARCYGCTCACT 959

Qy        935 CCTCCAGGGCACTTTTAGG-AAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGAC 993
              ||||||||:|||||||||  ||:|||||||||||||||||||||||||||||||||||||
Db        960 CCTCCAGGGSACTTTTAGGRAARGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGAC 1019

Qy        994 CTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCC 1053
              |||| :|||||||||||||:| ||:||| ||:|:||:| |||::|:||| | | || |:||
Db       1020 CTCA-VCCCGCCTGCAGTKGGTARAAG-CARCMGGKGGCCAWKTKCTAATTAAAAATKCC 1077

Qy       1054 TCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCA 1113
              | | |||:|||||||||||||  |||  : |||::: : : |: | |   || |:   |
Db       1078 TTAACTTYCCCCCGGCCCGGGGAAGGGGKGGGGRVSGKAWTTWTTTTTTTTTTTYAAAAA 1137

Qy       1114 AA 1115
              |:
Db       1138 AW 1139


RESULT 9
AL558892
LOCUS       AL558892               1093 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL558892 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
            Homo sapiens cDNA clone CS0DJ007YO09 5-PRIME, mRNA sequence.
ACCESSION   AL558892
VERSION     AL558892.2  GI:31283025
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1093)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
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COMMENT     On Feb 15, 2001 this sequence version replaced gi:12903858.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            8916.f For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DJ007AH05QP1&cluster=8916.f. Contact :
            Feng-Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DJ007AH05QP1.
FEATURES              Location/Qualifiers
     source           1. .1093
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DJ007YO09"
                      /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
                      /cell_line="JURKAT"
                      /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                      10-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           62.3%;  Score 942.4;  DB 9;  Length 1093;
  Best Local Similarity   94.2%;  Pred. No. 2.6e-158;
  Matches 1006;  Conservative   13;  Mismatches   20;  Indels   29;  Gaps    3;

Qy         29 CGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGG 88
              ||| |   |||  ||||||||||||||| |||||||||||||||||||||||||||||||
Db         43 CGGAATTCCCGGGATCGGCGACATGGAGAACGGGGCCTACGGCGCGGCCAAGGCGGGCGG 102

Qy         89 CTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTT 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 CTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTT 162

Qy        149 GGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGA 222

Qy        209 GTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 GTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGC 282

Qy        269 CATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCC 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCC 342

Qy        329 CCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGC 388
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        343 CCAGATCAGCAACGCCACTGACCGCMAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGC 402

Qy        389 TCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCAC 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCAC 462

Qy        449 CAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTT 508
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Db        463 CAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTT 521

Qy        509 CTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGG 568
              ||||||||||||||||                          ||||||||||||||||
Db        522 CTTTTCCATCTTCTCCTG--------------------------GCGCTACAAGGCTGG 554

Qy        569 CGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGC 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 CGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGC 614

Qy        629 CTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGA 688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        615 CTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCARAACGCGGA 674

Qy        689 GACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGG 748
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        675 GACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGG 734

Qy        749 GACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGC 808
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        735 GACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGC 794

Qy        809 CCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC 868
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 CCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC 854

Qy        869 TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGC-TTCAGTCAGCC 927
              |||||||||||||:|||||||||||||||||||||||||||||||| ||||||||:||
Db        855 TGGCGGGGGCTGGSAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTTCAGTCARCC 914

Qy        928 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTT 987
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Db        915 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTYCTCGCTTTT 974

Qy        988 AATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACA 1047
              :|||||:|||:|||||||||||||||||:||||:|||||||||||||||||||||:|
Db        975 WATGACMTCARCCCCGCCTGCAGTGGCTARAAGCBAGCAGGTGCCCATGTGCTACTGAMA 1034

Qy       1048 AGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTAT 1095
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Db       1035 AGTGCCTCARCTTCCCCCCGGCCCGGGTMAGGCGTGGGAGCGCTATAT 1082

RESULT 10
BM550919
LOCUS       BM550919               1031 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6584934 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471858
            5', mRNA sequence.
ACCESSION   BM550919
VERSION     BM550919.1  GI:18787506
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1031)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1980  row: p  column: 03
            High quality sequence stop: 653.
FEATURES              Location/Qualifiers
     source           1. .1031
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5471858"
                      /tissue_type="amelanotic melanoma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_41"
                      /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Library constructed by Ling Hong in the
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laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 62.0%; Score 937; DB 12; Length 1031;
Best Local Similarity 96.8%; Pred. No. 2.4e-157;
Matches 998; Conservative 0; Mismatches 27; Indels 6; Gaps 4;

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Qy        106 GCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCG 165
Db         61 GCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCG 120

Qy        166 TGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACT 225
Db        121 TGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACT 180

Qy        226 GCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCT 285
Db        181 GCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCT 240

Qy        286 TCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCA 345
Db        241 TCCTGGCCTCGGCTTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCA 300

Qy        346 CTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGT 405
Db        301 CTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGT 360

Qy        406 GGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGC 465
Db        361 GGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGC 420

Qy        466 TGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCT 525
Db        421 TGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCT 480

Qy        526 GGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCC 585
Db        481 GGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCC 540

Qy        586 AGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCAT 645
Db        541 AGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCAT 600

Qy        646 CTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACC 705
Db        601 CTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACC 660

Qy        706 AGCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCC 765
Db        661 AGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCC 720

Qy        766 CCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGT 825
Db        721 CCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGGACTGCCAGCCCCTCTCTTTCACCTGT 780

Qy        826 TCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC--TGGCGGGGGCTGGCA 883
Db        781 TCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCCTANCCCTGGCGGGGGGCTGGCA 840

Qy        884 GAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGG 943
Db        841 AAGCCACACCCCAAGTGCCTGTGCCCAGAAGGCTTCAGTCAGCCGCTCACTCCTCAGGGN 900

Qy        944 CACTTTTA--GGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCC 1001
Db        901 ACTTTTTAAGGAAAGGGTTTTTTAACTAATGTTTTTCCTCGCTTTTTATGACCTCAGCCC 960
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Qy       1002 CGCCTGCAG-TGGCTAGAAGCCAGCAGGTGCCCATGTG-CTACTGACAAGTGCCTCAGCT 1059
Db        961 CGCCTGGAGNTGGCTAGAAGCCAGCAGGGGCCCATGTGCCTACTGACAAGTGCCTCAACT 1020

Qy       1060 TCCCCCCGGCC 1070
Db       1021 CCCCCCCGGCC 1031
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RESULT 11
BM920554
LOCUS BM920554 1093 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6709586 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750562 5', mRNA sequence.
ACCESSION BM920554
VERSION BM920554.1 GI:19370933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1093)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12781 row: 1 column: 19
High quality sequence stop: 671.

FEATURES Location/Qualifiers
source 1. .1093
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750562"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 60.7%; Score 918.4; DB 12; Length 1093;
Best Local Similarity 94.1%; Pred. No. 5.1e-154;
Matches 1010; Conservative 0; Mismatches 52; Indels 11; Gaps 5;

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Qy         49 ACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCT 108
Db         20 ACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCT 79

Qy        109 TCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGT 168
Db         80 TCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGT 139

Qy        169 TCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCG 228
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Qy        229 TGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCC 288
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Db        200 TGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCC 259

Qy        289 TGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTG 348
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Db        260 TGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTG 319

Qy        349 ACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGT 408
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Db        320 ACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGT 379

Qy        409 TTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGG 468
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Db        380 TTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGG 439

Qy        469 TGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGG 528
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Db        440 TGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGG 499

Qy        529 GTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGA 588
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Db        500 GTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGA 559

Qy        589 ATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTG 648
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Db        560 ATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTG 619

Qy        649 TGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGC 708
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Db        620 TGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGC 679

Qy        709 CGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCT 768
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        680 CGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCT 739

Qy        769 CTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCC 828
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Db        740 CTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCC 799

Qy        829 ATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGG--CTGGCAGAG 886
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Db        800 ATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAACCTGGCGGGGGGCTGGCAAAGC 859

Qy        887 CCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCAC 946
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Db        860 CCACCCCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGNCGCTCACTCCTCAGGGCACC 919

Qy        947 TTTTAGGAAAGGGTTTTTAGCT-AGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCC--G 1003
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Db        920 TTTTAAGAAAGGGTTTTTACCTAAGGGTTTTTCCTCGCTTTTAATGACCTCAACCCCCGC 979

Qy       1004 CCTGCAGTGGCTAGAAGCCAGCAGGTGCCC-ATGTGCTACTGACAAGTGCCTCAGCTTCC 1062
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Db        980 CTGGAATGGGCTAAAAGCCACCAGGTGCCCAATGGGCTACTGAAAATGGCCTCAAGTTTC 1039

Qy       1063 CCCCGGCCCGGG-----TCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTG 1110
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RESULT 12
AL527114/c

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LOCUS       AL527114               1126 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL527114 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC019YE19 3-PRIME, mRNA sequence.
ACCESSION   AL527114
VERSION     AL527114.2  GI:31064968
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1126)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12790607.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC019AC10NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC019AC10NP1.
FEATURES             Location/Qualifiers
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                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             60.6%;  Score 915.8;  DB 9;  Length 1126;
  Best Local Similarity   90.9%;  Pred. No. 1.5e-153;
  Matches  990;  Conservative   20;  Mismatches   74;  Indels    5;  Gaps    4;

Qy        403 TGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACG 462
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Db       1090 TTTGMCTTRCTTTTTTTTTGTTTCTCTTCTCCCGCMCCCTTCCMMTCMCGAAGGGAAAGA 1031

Qy        463 TGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCT 522
               |   |  : |||  | :    | ||||  |||  ||||||  :|||||||||||||:|||||
Db       1030 SGGGGTGKTGGGGCCRACTTTGAGAGCACCCATCACTYCAGCTTCTTTTCCWTCTTCT 971

Qy        523 CCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCA 582
              |||:|||||||||||||:|||||| ||||||||||||||| ||||||||||||||||||||
Db        970 CCTKGGGTGTGCTGGCYCCCTGTCCTACCAGCGCTACAAAGCTGGCGTGGACGACTTCA 911

Qy        583 TCCAGAATTACGTTGACCCCACTCCGGA-CCCCAACACTGCCTACGCCTCCTA-CCCAGG 640
              |||||||||||||||||||||||||||:| ||||||||||||||||||||||| ||||||
Db        910 TCCAGAATTACGTTGACCCCACTCCGSACCCCCAACACTGCCTACGCCTCCTACCCCAGG 851

Qy        641 TGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGG 700
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Db        850 KGCATCTGTGAACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGA-GG 792

Qy        701 CTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGC 760
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Db        791 CTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGAACAGAGAGGGC 732

Qy        761 CCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCA 820
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Db        731 CCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCA 672

Qy        821 CCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTG 880
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Db        671 CCTGTTCCATCCTGTGCAGCTAACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTG 612

Qy        881 GCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCA 940
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Db        611 GCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCTGCTCACTCCTCCA 552

Qy        941 GGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCC 1000
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Db        551 GSGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTCCCTCGCTTTTAATGACCTCAGCC 492

Qy       1001 CCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTT 1060
              ||:|||||||||||||||||||||||||||||||||||||||||||| |||||||:|||||||||
Db        491 CCSCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTCACAAGTSCCTCAGCTT 432

Qy       1061 CCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTC 1120
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Db        431 CCCCCCGGCCCGGGTCAGGCCGTGGGAGTCGCTATTATCTGCGTTCTCTGCCAAAGACTC 372

Qy       1121 GTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACT 1180
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Db        371 GTGGGGGCCATCACACCTGCCCTGTGCAGCGGASCCGGACCASGCTCTTGTGTCCTCACT 312

Qy       1181 CAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT 1240
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Db        311 CAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT 252

Qy       1241 GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCT 1300
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Db        251 GGCCTCTGGGCTSCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCT 192

Qy       1301 TGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAAT 1360
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Db        191 TGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAAT 132

Qy       1361 ATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGAC 1420
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Db        131 ATTCTGCAGTTGTNACTTAGGAAGCCTGGGGAGGGCGGGGGTGCCCCATGGCTCCCAGAC 72

Qy       1421 TCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTT 1480
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Db          71 TCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGG--GNNTGCCCGGCTGGGNTGCTGTT 14

Qy       1481 TGGAGACGG 1489
              :|  :  ||
Db          13 KGNNBBGGG 5


RESULT 13
BM547376
LOCUS       BM547376               1047 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6507590 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724324
            5', mRNA sequence.
ACCESSION   BM547376
VERSION     BM547376.1  GI:18781091
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12713  row: g  column: 13
            High quality sequence stop: 675.
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5724324"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
ORIGIN

  Query Match             60.4%;  Score 913.6;  DB 12;  Length 1047;
  Best Local Similarity   94.6%;  Pred. No. 3.7e-153;
  Matches  990;  Conservative    0;  Mismatches   50;  Indels    7;  Gaps    4;

Qy         24 GGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 83
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Db          1 GGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 60

Qy         84 GGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 143
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Db         61 GGCGGCTCCTTCGACCTGCGGCGCTTCGTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 120

Qy        144 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCC 203
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Db        121 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGGTACAGCAATGCC 180

Qy        204 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 263
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Db        181 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 240

Qy        264 AGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTAT 323
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Qy        324 TTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTC 383
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Qy        384 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCA 443
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Db        361 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAGCCAGTGGGCA 420

Qy        444 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 503
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Db        421 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 480

Qy        504 AGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 563
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Db        481 AGCTTCTTTTCCATCTTCTCCTGNGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 540

Qy        564 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 623
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Db        541 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 600

Qy        624 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 683
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Db        601 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 660

Qy        684 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGA 743
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Db        661 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGA 720

Qy        744 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTG 803
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        721 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTG 780

Qy        804 CCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCA 863
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAGCCCCTCTCTTTTCACTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCA 840

Qy        864 TAGCC-TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGT 922
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Db        841 TAACCTTGGCGGGGGCTGGCAAAACCACACCCCAAGTGCCTGTGGCCAGAGGGCTTTAGT 900

Qy        923 CAGCCGCTCACTCCTCCAGGGCAC--TTTTAGGAAAGGGTTTTTAGCT-AGTGTTTTTCC 979

Db        901 TAACCGCTCAATCCTCCAGGGAACTTTTTTAGGAAGGGTTTTTTACCTAAGGGTTTTCCC 960

Qy        980 TCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGG---CTAGAAGCCAGCAGGTGCCCATG 1036

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Qy       1037 TGCTACTGACAAGTGCCTCAGCTTCCC 1063

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RESULT 14
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DEFINITION  AL571941 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
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ACCESSION   AL571941
VERSION     AL571941.2  GI:31293331
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12929733.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI029AC03NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI029AC03NP1.
FEATURES             Location/Qualifiers
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                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           60.2%;  Score 910.2;  DB 9;  Length 1201;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-152;
  Matches  935;  Conservative    6;  Mismatches   30;  Indels    1;  Gaps    1;

Qy        506 CTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGC 565

Db        971 CTTCAGCTYTTTCCATCTCTCCTGGGTGGGCTGCCTCCCTGCCTACCAGCGCTACAAGGC 912

Qy        566 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 625

Db        911 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 852

Qy        626 CGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGC 685

Db        851 CGCCTCCTACCCAGGTGCATCTGT-GACAACTACCAACAGCCACCCTTCACCCAGAACGC 793

Qy        686 GGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAG 745

Db        792 GGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAG 733

Qy        746 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCC 805

Db        732 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGGACTGCC 673

Qy        806 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 865

Db        672 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 613

Qy        866 GCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAG 925

Db        612 GCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAG 553

Qy        926 CCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTT 985

Db        552 CCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTT 493

Qy        986 TTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGA 1045

Db        492 TTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGA 433

Qy       1046 CAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTT 1105

Db        432 CAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTT 373

Qy       1106 CTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGC 1165

Db        372 CTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGC 313

Qy       1166 TCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCA 1225

Db        312 TCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCA 253

Qy       1226 CCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTC 1285

Db        252 CCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTC 193

Qy       1286 ATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACC 1345

Db        192 ATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACC 133

Qy       1346 CAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCC 1405

Db        132 CAGCTTTATGTAAATATTCTGCAGTTGTNACTTAGGAAGCCTGGGGAGGGCAGGGGTGCC 73

Qy       1406 CCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCG 1465

Db          72 CCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATRMAMG 13

Qy       1466 GCCTGGGATGCT 1477

Db          12 GMATGRGATGAT 1


RESULT 15
AL546400
LOCUS       AL546400               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL546400 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI031YC02 5-PRIME, mRNA sequence.
ACCESSION   AL546400
VERSION     AL546400.2  GI:31268234
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
```

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  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12879477.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI031BB01QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI031BB01QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
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                      /clone="CS0DI031YC02"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             59.9%;  Score 905.8;  DB 9;  Length 1201;
  Best Local Similarity   97.3%;  Pred. No. 9.4e-152;
  Matches  937;  Conservative    5;  Mismatches   17;  Indels    4;  Gaps    2;

Qy         24 GGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 127

Qy         84 GGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 143
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        128 GGCGGCTCCTTCGACCTGCGGCGCTTCGTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 187

Qy        144 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCC 203
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        188 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGGTACAGCAATGCC 247

Qy        204 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 307

Qy        264 AGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTAT 323
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        308 AGTGCCATCGGGGTGCTGGCMTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTAT 367

Qy        324 TTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTC 383
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 TTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTC 427

Qy        384 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCA 443
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCA 487

Qy        444 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 503
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 547

Qy        504 AGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 563
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Db        548 AGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 607

Qy        564 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 667

Qy        624 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 683
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 727

Qy        684 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGA 743
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        728 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGA 787

Qy        744 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTG 803
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        788 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTG 847

Qy        804 CCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCA 863
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 CCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCA 907

Qy        864 TAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTC 923
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        908 TAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTT 966

Qy        924 AGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGC 983
              |||||||||||||||| |||   :  ||   | || || ||||::|||||||||||||  |
Db        967 AGCCGCTCACTCCTCAAGG---SACTTTAGGAAAGGGTTTTWRCTAGTGTTTTTCTCCCT 1023

Qy        984 TTT 986
              |||
Db       1024 TTW 1026


RESULT 16
AL562951/c
LOCUS       AL562951                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL562951 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC026YD11 3-PRIME, mRNA sequence.
ACCESSION   AL562951
VERSION     AL562951.2  GI:31286958
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12911883.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            8916.f For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC026CB06NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC026CB06NP1.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
                      /clone="CS0DC026YD11"
                      /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             59.9%;  Score 905.8;  DB 9;  Length 1201;
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  Best Local Similarity   95.9%;  Pred. No. 9.4e-152;
  Matches  919;  Conservative   12;  Mismatches   26;  Indels    1;  Gaps    1;

Qy        537 GCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTT 596
              ||||||||||||||||||:|| |||||||||||||| || |||||||:|:||| |||||
Db        959 GCCTCCCTGGCCTACCAGSGCAACAAGGCTGGCGTGAACAACTTCATCMARAATAACGTT 900

Qy        597 GACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAAC 656
              |||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Db        899 GACCCCACTCCGGACCCCAAAACTGCCTACGCCTCCTACCCAGGTGCATCTGT-GACAAC 841

Qy        657 TACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCT 716
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 TACCGACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCT 781

Qy        717 GTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTG 776
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Db        780 GTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGAACAGAGAGGGCCCTCCCCTCTGCCCTG 721

Qy        777 GACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTG 836
              |||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db        720 GACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTCTCACCTGTTCCATCCTGTG 661

Qy        837 CAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCA 896
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Db        660 CAGCTAACACACAGCTAAGGAGCCTCATARCCTGGCGGGAGCTGGCAGAGCCACACCCCA 601

Qy        897 AGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAA 956
              ||||||||||||||||||:|||||||| ||||||||||||||||||||||||||||||
Db        600 AGTGCCTGTGCCCAGAGGGCWTCAGTCAGCNGCTCACTCCTCCAGGGCACTTTTAGGAAA 541

Qy        957 GGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTA 1016
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        540 GGGTTTTTAGCTAGTGTTTTACCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTA 481

Qy       1017 GAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTC 1076
              |||||||||||||||||||| |||:|||||||||||||||||||||||||||||||||||
Db        480 GAAGCCAGCAGGTGCCCATGTGCNACTRACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTC 421

Qy       1077 AGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACAC 1136
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        420 AGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAARACTCGTGGGGGCCATCACAC 361

Qy       1137 CTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCT 1196
              ||||||||||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db        360 CTGCCCTGTGCAGCGGAGCCGGACCAGGSTCTTGTGTCCTGACTCAGGTTTGCTTCCCCT 301

Qy       1197 GTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCT 1256
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        300 GTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCSTCTGGGCTGCCT 241

Qy       1257 CCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGC 1316
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Db        240 CCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTGGCTCCCACCCCTGGC 181

Qy       1317 AGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTAC 1376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTAC 121

Qy       1377 TTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGT 1436
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Db        120 TTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGT 61

Qy       1437 GTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAA 1494
              |||||||||||||||||||||||||||||||||||||||||||  : : : |  ||
Db         60 GTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTSNNADNHDDAATAAA 3


RESULT 17
AL557237
LOCUS       AL557237               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL557237 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
            clone CS0DH004YL10 5-PRIME, mRNA sequence.
ACCESSION   AL557237
VERSION     AL557237.2  GI:31279037
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12900646.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            8916.f For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DH004DF05QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DH004DF05QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DH004YL10"
                     /tissue_type="T CELLS (JURKAT CELL LINE)"
                     /cell_line="JURKAT CELL LINE"
                     /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match           59.9%;  Score 905.2;  DB 9;  Length 1201;
  Best Local Similarity   96.8%;  Pred. No. 1.2e-151;
  Matches  972;  Conservative    4;  Mismatches   22;  Indels    6;  Gaps    5;

Qy         17 CGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGC 76
              | ||| |  | | |  ||||||||||||||||||||||||||||||||||||||||||
Db         57 CCCGGGATGGCGGCGGCACGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGC 116

Qy         77 CAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGG-TGGCGC 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        117 CAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTTGGCGC 176

Qy        136 GCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 GCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACA 236

Qy        196 GCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCC 255
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Db        237 GCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCC 296

Qy        256 GCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCG 315
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Db        297 GCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCG 356

Qy        316 ACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACC 375
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Db        357 ACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACC 416

Qy        376 TGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACC 476

Qy        436 AGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCA 495
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Db        477 AGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCA 535

Qy        496 TCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGC 555

Db        536 TCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGC 595

Qy        556 GCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCA 615

Db        596 GCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCA 655

Qy        616 ACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCA 675

Db        656 ACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCA 715

Qy        676 CCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTA 735

Db        716 CCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTA 775

Qy        736 GCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCC 795

Db        776 GCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCC 835

Qy        796 TGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAG 855

Db        836 TGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAG 895

Qy        856 GAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGG 915

Db        896 GAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCTGTGCCCAGAGGS 954

Qy        916 CTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTT 975

Db        955 TTTCAGTCAGCTGCTCACTCCTCCAGGGCACTTTTARGAAAGGGTTTTTAGCTAGTGTTT 1014

Qy        976 TTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAA 1019

Db       1015 TT-CTCGCTTTTAATGAC--TCAGCCCGCCTGCAATGGTAARAR 1055
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RESULT 18
AL571749/c
LOCUS       AL571749               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL571749 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI031YC02 3-PRIME, mRNA sequence.
ACCESSION   AL571749
VERSION     AL571749.2  GI:31293140
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12929355.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI031BB01NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI031BB01NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI031YC02"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           59.8%;  Score 904.6;  DB 9;  Length 1201;
  Best Local Similarity   96.1%;  Pred. No. 1.5e-151;
  Matches  947;  Conservative   10;  Mismatches   24;  Indels    4;  Gaps    3;

Qy        467 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 526

Db       1016 GGCTGTKGGGCCSACTYTTTAGGCAGCCATCACC-TCMGCTTYTTTCCCATCTTCTCYTG 958

Qy        527 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 586

Db        957 GG--TGKGYTGCCTCCCTGGCCTACCAGCGCTACAAYGCTGGCGTGGACGACTTCATCCA 900

Qy        587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646

Db        899 RAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 840

Qy        647 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 706

Db        839 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 780

Qy        707 GCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 766

Db        779 GCCGCCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGA-GGCCCTCCC 721

Qy        767 CTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTT 826

Db        720 CTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTT 661

Qy        827 CCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG 886

Db        660 CCATCCTGTGCAGCTAACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG 601

Qy        887 CCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCAC 946

Db        600 CCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCAC 541

Qy        947 TTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCT 1006

Db        540 TTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCT 481

Qy       1007 GCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCC 1066

Db        480 GCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCC 421

Qy       1067 GGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGG 1126

Db        420 GGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGG 361

Qy       1127 GCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTT 1186

Db        360 GCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTT 301

Qy       1187 TGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTC 1246

Db        300 TGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTC 241

Qy       1247 TGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCC 1306

Db        240 TGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCC 181

Qy       1307 CACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTG 1366

Db        180 CACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTG 121
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Qy       1367 CAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC 1426
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 CAGTTGTAACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC 61

Qy       1427 TGTGCCGAGTGTATTATAAAATCGT 1451
             |||:||||||:|||||||||| | |
Db         60 TGTSCCGAGTSTATTATAAAAACAT 36


RESULT 19
AL545227
LOCUS       AL545227                1001 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL545227 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI028YB09 5-PRIME, mRNA sequence.
ACCESSION   AL545227
VERSION     AL545227.2  GI:31267063
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12877708.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI028CA05QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI028CA05QP1.
FEATURES              Location/Qualifiers
     source           1. .1001
                      /organism="Homo sapiens"
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                      /db_xref="taxon:9606"
                      /clone="CS0DI028YB09"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           59.4%;  Score 898.4;  DB 9;  Length 1001;
  Best Local Similarity  98.8%;  Pred. No. 1.9e-150;
  Matches  925;  Conservative    1;  Mismatches    7;  Indels    3;  Gaps    2;

Qy         37 GCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCG 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCG 128

Qy         97 ACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCG 156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCG 188

Qy        157 CCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGC 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGC 248

Qy        217 AGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGG 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGG 308

Qy        277 TGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCA 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCA 368

Qy        337 GCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGA 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGA 428

Qy        397 CCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGA 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGA 488

Qy        457 AGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCA 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 AGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCA 548

Qy        517 TCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 TCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACG 608

Qy        577 ACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACC 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACC 668

Qy        637 CAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG 728

Qy        697 AGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGA 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 AGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGA 788

Qy        757 GGGCCCTCCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCT 816
              ||| |||||||||||||||||||||||||||          ||||||||||||||||||||||||||
Db        789 GGG-CCTCCCCCTCTGCCCTGGACTTTCC--ATGAGCTCCTGGAACTGCCAGCCCCTCTCT 845

Qy        817 TTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGG 905

Qy        877 GCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCC 936
              ||||||||||||||||||||||||||||||||||||||||||: ||||||||||||||||||
Db        906 GCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGSTTTCAGTCAGCCGCTCACTCC 965

Qy        937 TCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTG 972
              ||||||||||||||||||||||||||||||||||||
Db        966 TCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTG 1001


RESULT 20
AL556778
LOCUS       AL556778                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL556778 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK005YL09 5-PRIME, mRNA sequence.
ACCESSION   AL556778
VERSION     AL556778.2  GI:31278579
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12899769.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
```

```
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK005CF05QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK005CF05QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DK005YL09"
                      /cell_type="HELA CELLS COT 25-NORMALIZED"
                      /cell_line="HELA"
                      /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             59.3%;  Score 896.8;  DB 9;  Length 1201;
  Best Local Similarity   96.5%;  Pred. No. 3.8e-150;
  Matches  963;  Conservative    6;  Mismatches   23;  Indels    6;  Gaps    5;

Qy         17 CGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGC 76
              | ||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CCCGGGATGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGC 119

Qy         77 CAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCG 136
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        120 CAAGGCGGGCGGCTCCTTCRACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCG 179

Qy        137 CGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAG 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAG 239

Qy        197 CAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCG 299

Qy        257 CTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCT--CGGCCTTCTTCTTGGTGGTC 314
              |||||||||||||||||||||||||||||||||||||    | ||||||||||||||||||
Db        300 CTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTACGGACCTTCTTCTTGGTGGTC 359

Qy        315 GACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGAC 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGAC 419

Qy        375 CTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAAC 434
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        420 CTGCTCTTCTCAGCTCTCTGGACCTTCCTGTRGTTTGTTGGTTTCTGCTTCCTCACCAAC 479

Qy        435 CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCC 494
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        480 CAGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCC 538

Qy        495 ATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 ATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAG 598

Qy        555 CGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCC 614
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Db        599 CGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCC 658

Qy        615 AACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 AACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTC 718

Qy        675 ACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTT 734
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        719 ACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTT 778

Qy        735 AGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTC 794
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        779 AGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTC 838

Qy        795 CTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAA 898

Qy        855 GGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACAC-CCCAAGTGCCTGTGCCCAGAG 913
              |||::|||||||| ||||||||||||||||||||  :|| ||||||||||||||||||||
Db        899 GGARSCTCATAGCTTGGCGGGGGCTGGCAGAGCACMACACCCAAGTGCCTGTGCCCAGAG 958

Qy        914 GGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 973
              || ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        959 GGTTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGG-TTTTAGCTAGTGT 1017

Qy        974 TTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGT 1011
              |||| ||||||||||||||||     || |  | |  :|
Db       1018 TTTT-CTCGCTTTTAATGACTCAGCCCGCTKCAGTGST 1054


RESULT 21
AL573863/c
LOCUS       AL573863               1100 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL573863 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI054YK18 3-PRIME, mRNA sequence.
ACCESSION   AL573863
VERSION     AL573863.2  GI:31295199
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12933514.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI054BF09NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI054BF09NP1.
FEATURES              Location/Qualifiers
     source           1. .1100
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI054YK18"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             59.3%;  Score 896.6;  DB 9;  Length 1100;
  Best Local Similarity   94.8%;  Pred. No. 4.1e-150;
  Matches  978;  Conservative   18;  Mismatches   28;  Indels    8;  Gaps    7;

Qy        451 ACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCT 510
              :|||    || |  :|  || ||| | : :   ||||||:|  ||||||||||||||| :
Db       1027 MCCCACCCGAAGACSTCTTGTGGGGCCRAYTCTTGAGGGMACNCATCACCTTCAGCTT-Y 969

Qy        511 TTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCG 570
              |||||||||||||||||: |   : |:||||||||||||||:||||:||||||||||
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```
Db        968 TTTCCATCTTCTCCTGGGKGGG--YTGSCTCCCTGGCCTACCAGSGCTAMAAGGCTGGCG 911

Qy        571 TGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCT 630
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        910 TGGACGACTTCATCCAGAATTAC-TTGACCCCACTCCGGACCCCAACACTGCCTACGCCT 852

Qy        631 CCTACCCAGGTGCATCTGTGGACAACTACC-AACAGCCACCCTTCACCCAGAACGCGGAG 689
              |:|||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||
Db        851 CYTACCCAGGTGCATCTGTGAACAACTACCYAACAGCCACCCTTCACCCAGAACGCGGAG 792

Qy        690 ACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGG 749
              |||||||| ||:||||||||||||||||||||||||| ||||||||||||||||||||||
Db        791 ACCACCGA-GGYTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGG 733

Qy        750 ACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCC 809
              |||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Db        732 ACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGNACTGCCAGCC 673

Qy        810 CCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCT 869
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        672 CCTCTCTTTCACYTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCT 613

Qy        870 GGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGC 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGC 553

Qy        930 TCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAA 989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAA 493

Qy        990 TGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAG 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 TGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAG 433

Qy       1050 TGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCT 1109
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        432 TGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTNTCT 373

Qy       1110 GCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTT 1169
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||:||||
Db        372 GCCAAAGACTCGTGGGGGCCATCACACNTGCCCTGTGCAGCGGAGCCGGACCAGGBTCTT 313

Qy       1170 GTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCAC 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCAC 253

Qy       1230 CCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGG 193

Qy       1290 CACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGC 1349
              |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        192 CACTTCCTCCTTGCTCCCACCCCTGGCRGCAGGGAAGGGCTTTGCCTGACAACACCCAGC 133

Qy       1350 TTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCAT 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCAT 73

Qy       1410 GGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAA-TCGTGGGGGAGATGC-CCGGC 1467
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||||
Db         72 GGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAANTCGTGGGGGAGATGCNCCGGC 13

Qy       1468 CTGGGATGCTGT 1479
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Db         12 NTGGGATGSTGK 1
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RESULT 22
BX377649/c
LOCUS   BX377649   1201 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX377649 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI009YI04 3-PRIME, mRNA sequence.
ACCESSION   BX377649
VERSION   BX377649.1 GI:30450591
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI009BE02NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI009BE02NP1.
FEATURES   Location/Qualifiers
     source   1. .1201
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="CS0DI009YI04"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match   59.2%; Score 894.6; DB 13; Length 1201;
  Best Local Similarity   89.0%; Pred. No. 9.5e-150;
  Matches 957; Conservative   40; Mismatches   73; Indels   5; Gaps   4;

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Qy        395 GACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGCAGTCACCAACCC 454
              ||||||||||||:|||||||  ||   :||||||||||||:|| |||:|||:|:||||:
Db       1070 GACCTTCCTGTGKTTTGTTG--TTTCTSTTCCTCACCAACCMGT-GGCMGTCMCMAACCM 1014

Qy        455 GAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTC 514
               ||||||||||||| ||||::|||||||||:||||| ||||||:||||| |||||||||
Db       1013 AAAGGACGTGCTGGT-GGGGMMGACTCTGTRAGGGCGGCCATCMCCTTCGGCTTCTTTTC 955

Qy        515 CATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGA 574
              |:|||||||:|||:|:|  |     |     ||:|:|:||    |:||:|||||||||||||
Db        954 CWTCTTCTCCKGGGKTKTTTTTTTTTTTTTGKCYTWCCTTTGMTAMAAGGCTGGCGTGGA 895

Qy        575 CGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA 634
              :||||::||: |:||||||||||||:|||||||||||||||| || |||:||||||||:|
Db        894 MGACTWMATMAARAATTACGTTGMCCCCACTCCGGACCCAAAAAACTGCMTACGCCTCMTA 835

Qy        635 CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCAC 694
              ||||||||||||||::|:|||||||||||||||||||||||||:||||||||||||||||
Db        834 CCCAGGTGCATCTGTRRAMAACTACCAACAGCCACCCTTCACCMAGAACGCGGAGACCAC 775

Qy        695 CGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGA 754
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||| | |:|
Db        774 CGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTYGCGTGGGAAGGGGAAAARA 715

Qy        755 GAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCT 814
              ||||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||
Db        714 GAGGGCCCTCCCCTCTGCCCTGRACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCT 655

Qy        815 CTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGG 874
              |||||||||||||||||||||| ||||:||||||||||||||||||||:|||||||||||
Db        654 CTTTCACCTGTTCCATCCTGTGCTGCTGAMACACAGCTAAGGAGCCTMATAGCCTGGCGG 595

Qy        875 GGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACT 934
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Db        594 GGGCTGGCAGCGCCACACCCCCTGTGCCTGTGCCCAGAGGGCTTCAGTCCGCCGCTCTCT 535

Qy        935 CCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACC 994

Db        534 CCTCCCGGGCCCTTTTAGGAAAGGGTTTTTCGCTTGTGTTTTTCCTCGCTTTTTATGTCC 475

Qy        995 TCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT 1054

Db        474 TCCGCCCCGCCTGCCGTGGCTCGACGCCCGCCGGTGCCCCTGTGCTCCTGCCCAGTGCCT 415

Qy       1055 CAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAA 1114

Db        414 CCGCTTCCCCCCGGCCCGGGTCCGGCCGTGGGGGCCGCTGTTGTCTGCGTTCTCTGCCAN 355

Qy       1115 AGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTC 1174

Db        354 NGNCTCGTGGGGGCCNTCACCCCTGCCCTGTGCCGCGGCGCCGGCCCAGGCTCTTGTGTC 295

Qy       1175 CTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGT 1234

Db        294 CTCCCTCCGGTTTGCTTCCCCTGTGCCCACTGCTGTCTGCTCTGGGGGCCCCCCCCCCTGT 235

Qy       1235 GCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTT 1294

Db        234 GCCGGTGGCCTCTGGGCTSCCTCCCSTGGTGTGTGGGCGGGGCTGGTGCTCTTGGCCCTT 175

Qy       1295 CCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTAT 1354

Db        174 CCTCCTTGCTCCCCCCCCTGGCCGCAGGGAAGGGCTTTGCCTGACAACACCCCGCTTTAT 115

Qy       1355 GTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTC 1414

Db        114 GTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCA-GGGTGCCCCATGGCTC 56

Qy       1415 CCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCT 1469

Db          55 CCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGMMT 1


RESULT 23
AL527971
LOCUS       AL527971               1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL527971 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC027YP17 5-PRIME, mRNA sequence.
ACCESSION   AL527971
VERSION     AL527971.2  GI:31065822
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12791464.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC027CH09QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC027CH09QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DC027YP17"
                      /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             59.1%;  Score 894.2;  DB 9;  Length 1201;
  Best Local Similarity   98.1%;  Pred. No. 1.1e-149;
  Matches  962;  Conservative    5;  Mismatches    8;  Indels    6;  Gaps    6;

Qy         22 GGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGG 81

Db         94 GCGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGG 153

Qy         82 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 141

Db        154 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 213

Qy        142 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 201

Db        214 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 273

Qy        202 CCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 261

Db        274 CCCACGAKTCTAAGCAGATKTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 333

Qy        262 GCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT 321

Db        334 GCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT 393

Qy        322 ATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCT 381

Db        394 ATTTCCCCCAGAWCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCT 453

Qy        382 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 441

Db        454 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 513

Qy        442 CAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 501

Db        514 CAGTCACCAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 572

Qy        502 TCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 561

Db        573 TCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 632

Qy        562 AGGCTGGCGTGGACGACTTCATCCAGAAT-TACGTTGACCCCACTCCGGACCCCAACACT 620

Db        633 AGGCTGGCGTGGACGACTTCATCCAGAATATACGTTGACCCCACTCCGGACCCCAACACT 692

Qy        621 GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAG 680

Db        693 GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAG 752

Qy        681 AACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTG 740

Db        753 AACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTG 812

Qy        741 GGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAA 800

Db        813 GGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAA 872

Qy        801 CTGCCAGCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCC 860

Db        873 CTGCCAGCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCC 932

Qy        861 TCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCA 920

Db        933 TCATAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCTGTGCCCAGA-GGCTTCA 990
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Qy        921 GTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTTCCT 980
              |||||| |||||||||||||||||||||||||||||||| |||||||||||| ||||:||
Db        991 GTCAGCTGCTCACTCCTCCAGGGCACTTTTAGGAAAGGG-TTTTAGCTAGTG-TTTTYCT 1048

Qy        981 CGCTTTTAATGACCTCAGCCC 1001
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Db       1049 CGCTTTTAATGACYCAGCCCC 1069


RESULT 24
BM923973
LOCUS       BM923973                 981 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6709776 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760126
            5', mRNA sequence.
ACCESSION   BM923973
VERSION     BM923973.1  GI:19374352
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12806  row: k  column: 07
            High quality sequence stop: 705.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5760126"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             59.1%;  Score 893.8;  DB 12;  Length 981;
  Best Local Similarity   96.3%;  Pred. No. 1.2e-149;
  Matches  945;  Conservative    0;  Mismatches   31;  Indels    5;  Gaps    3;

Qy        318 GCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTG 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTG 60

Qy        378 CTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAG 120

Qy        438 TGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATC 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATC 180

Qy        498 ACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGC 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGC 240

Qy        558 TACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAAC 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAAC 300

Qy        618 ACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACC 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACC 360

Qy        678 CAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGC 737
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        361 CAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGC 420

Qy        738 GTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTG 797
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        421 GTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTG 480

Qy        798 GAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGA 857
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Db        481 GAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGA 540

Qy        858 GCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCT 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCT 600

Qy        918 TCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTTAGCTAGTGTTTTT 977
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Db        601 TCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTTAGCTAGTGTTTTT 660

Qy        978 CCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGT 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGT 720

Qy       1038 GCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTA 1097
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 GCTACTGACAAGTGCCTCAGCTT-CCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTA 779

Qy       1098 TCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCG 1157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 TCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCG 839

Qy       1158 GACCAGGCTCTTGT-GTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTAT---G 1213
              |||||||||||||| |||||||||||||||||  | ||||||||||||||||||   |
Db        840 GACCAGGCTCTTGTGGTCCTCACTCAGGTTTGGCTTCCCTGTGCCCACTGCTGGNNATGA 899

Qy       1214 ATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCG 1273
              ||||||||| ||| |||||||||||||||||||||||| |  ||  | | | | |  |
Db        900 ATCTGGGGGGCACANCCCTGTGCCGGTGGCCTCTGGGCTGGCCTCCCCCGGGGGGGTNAG 959

Qy       1274 GGGCTGGTGCTCATGGCACTT 1294
              || | || |||  |||| | |
Db        960 GGCCGGGGGCTGGTGGCTCAT 980


RESULT 25
AL574399/c
LOCUS       AL574399                 1139 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  AL574399 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI058YI03 3-PRIME, mRNA sequence.
ACCESSION   AL574399
VERSION     AL574399.2  GI:31312717
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1139)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
```

```
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12934570.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI058AE02NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI058AE02NP1.
FEATURES              Location/Qualifiers
     source           1. .1139
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI058YI03"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             58.5%;  Score 885.2;  DB 9;  Length 1139;
  Best Local Similarity   94.4%;  Pred. No. 4.5e-148;
  Matches  953;  Conservative    5;  Mismatches   48;  Indels    4;  Gaps    4;

Qy        464 GCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTC 523
              || ||  || |  | | || || | |    |    ||||| ||||| |||||:|||||||
Db       1027 GCCGGGTGGTGGGGCCCCTTTGTGCGGSCGCCMTCCCTTCCGCTTC-TTTCCMTCTTCTC 969

Qy        524 CTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCAT 583
              |  |||    |   ||||||||||||:|||||| :| |:||||||||||| |||||||
Db        968 CCTGGGGTGGGCTGCCTCCCTGGCCTMCCAGCGCCMCCAVGCTGGCGTGGACAACTTCAT 909

Qy        584 CCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA-CCCAGGTG 642
              |||:|||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        908 CCARAATTACGTTGACCCCACTCCGGACCCCAATACTGCCTACGCCTCCTACCCCAGGTG 849

Qy        643 CATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCT 702
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 CATCTGTGAACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCT 789

Qy        703 ACCAGCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCC 762
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||||
Db        788 ACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGA-GGCCC 730

Qy        763 TCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACC 822
              |||||||||||||||||||||||| |||||||||| |||||||||||||||||| |||||
Db        729 TCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGNACTGCCAGCCCCTCTCTCTCACC 670

Qy        823 TGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGC 882
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        669 TGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCT-GC 611

Qy        883 AGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGG 942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGG 551

Qy        943 GCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCC 1002
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        550 GCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTCCCTCGCTTTTAATGACCTCAGCCCC 491

Qy       1003 GCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCC 1062
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        490 GCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCNACTGACAAGTGCCTCAGCTTCC 431

Qy       1063 CCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGT 1122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGT 371

Qy       1123 GGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCA 1182
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        370 GGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTAACTCA 311

Qy       1183 GGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGG 1242
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGG 251

Qy       1243 CCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG 1302
              |||||||||||||||||||||||||||||||||| |||||||||||  || ||| |
Db        250 CCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGNGCTCATGGCACTCCCCCCTCG 191

Qy       1303 CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATAT 1362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATAT 131

Qy       1363 TCTGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTC 1422
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TCTGCAGTTGTAACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTC 71

Qy       1423 TGTCTGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGG 1472
              |||||||||||||||||||||||||||  |||||||||||||||| |||
Db          70 TGTCTGTGCCGAGTGTATTATAAAATCGNTGGGGAGATGCCCGGCCAGGG 21


RESULT 26
AL525578
LOCUS       AL525578                1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL525578 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC012YH07 5-PRIME, mRNA sequence.
ACCESSION   AL525578
VERSION     AL525578.2  GI:31063442
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12789071.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC012CD04QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC012CD04QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DC012YH07"
                      /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             57.5%;  Score 868.8;  DB 9;  Length 1201;
  Best Local Similarity   95.1%;  Pred. No. 3.9e-145;
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  Matches  934;  Conservative    5;  Mismatches   37;  Indels    6;  Gaps    4;

Qy         22 GGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGG 81
              ||  |||       |||   ||||||||||||||||||||||||||||||||||||||||
Db         49 GGTCCGGAATTCCCGGGATCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGG 108

Qy         82 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 168

Qy        142 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 228

Qy        202 CCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 CCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 288

Qy        262 GCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT 348

Qy        322 ATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCT 408

Qy        382 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 468

Qy        442 CAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 CAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 528

Qy        502 TCAGCTTCTTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 TCAGCTTCTTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 588

Qy        562 AGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTG 648

Qy        622 CCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGA 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGA 708

Qy        682 ACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGG 741
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 ACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGG 768

Qy        742 GAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCT-GGAA 800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 GAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGGAA 828

Qy        801 CTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCC 860
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        829 CTGCCAGCCCCTCTCTTTCACCTGTKCCATCCTGTGCAGCTGACACACAGCTAAGGAGCC 888

Qy        861 TCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCA 920
              |||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db        889 TCATAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCTGTGCCCAGA-GGCTTCA 946

Qy        921 GTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCT 980
              ||:||| |||||||||: ||   |  ||  | :| || ||||||||||||||  |
Db        947 GTYAGCTGCTCACTCCTCMGGG---CACTTTAGGRAAGGGTTTTAGCTAGTGTTTTCTCG 1003

Qy        981 CGCTTTTAATGACCTCAGCCCC 1002
              |  |: | |     | ||| |
Db       1004 CTTTWATGACTCAGCCCGCCGC 1025


RESULT 27
AL549812
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LOCUS       AL549812               1134 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL549812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI054YK18 5-PRIME, mRNA sequence.
ACCESSION   AL549812
VERSION     AL549812.2  GI:31271630
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1134)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12886163.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI054BF09QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI054BF09QP1.
FEATURES             Location/Qualifiers
     source          1. .1134
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI054YK18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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  Query Match             57.3%;  Score 865.8;  DB 9;  Length 1134;
  Best Local Similarity   95.8%;  Pred. No. 1.3e-144;
  Matches  926;  Conservative    5;  Mismatches   32;  Indels    4;  Gaps    4;

Qy         12 GCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGC 71
              || | |  ||   |   |||  |   |||   ||||||||||||||||||||||||||||
Db         35 GCAGGCTGGTACCGGTCCGGAATTCCCGGGATCGGCGACATGGAGAGCGGGGCCTACGGC 94

Qy         72 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 154

Qy        132 GCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 214

Qy        192 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 274

Qy        252 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTG 311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCTTTCTTCTTGGTG 334

Qy        312 GTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGT 371
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 GTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGT 394

Qy        372 GACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACC 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 GACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACC 454
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Qy        432 AACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCA 491
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        455 AACCAGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCA 513

Qy        492 GCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTAC 551
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        514 GCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCYGGCCTCCCTGGCCTAC 573

Qy        552 CAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGAC 611
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGAC 633

Qy        612 CCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCC 671
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCC 693

Qy        672 TTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCG 731
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        694 TTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCG 753

Qy        732 GTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGC 791
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        754 GTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGC 813

Qy        792 CTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGC 851
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 CTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGC 873

Qy        852 TAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAG 911
              |||||||||||||||||||||||| ||||  |  |||||||||||||||||||||||||||
Db        874 TAAGGAGCCTCATAGCCTGGCCGGGGGCTGGCAGAGCACACCCCAAGTGCCTGTGCCCAG 933

Qy        912 AGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGT 971
              |||| |||||||||||||||:|| :|||||:|||||||||||| ||||||||:|||||
Db        934 AGGG-TTCAGTCAGCCGCTCACYCC-YCAGGGSACTTTTAGGAAA-GGTTTTTARCTAGT 990

Qy        972 GTTTTTC 978
              |||||||
Db        991 TTTTTTC 997


RESULT 28
BM923138
LOCUS       BM923138                1069 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6631909 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5757122
            5', mRNA sequence.
ACCESSION   BM923138
VERSION     BM923138.1  GI:19373517
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1069)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12798  row: n  column: 03
            High quality sequence start: 10
            High quality sequence stop: 669.
FEATURES             Location/Qualifiers
     source          1. .1069
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5757122"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             56.9%;  Score 860.6;  DB 12;  Length 1069;
  Best Local Similarity   95.1%;  Pred. No. 1.1e-143;
  Matches  923;  Conservative    0;  Mismatches   39;  Indels    9;  Gaps    3;

Qy         51 ATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTC 110
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Db         21 ATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTC 80

Qy        111 CTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTC 170
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTC 140

Qy        171 TCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTG 230
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTG 200

Qy        231 TTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTG 290
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Db        201 TTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTG 260

Qy        291 GCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGAC 350
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Db        261 GCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGAC 320

Qy        351 CGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTT 410
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Db        321 CGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTT 380

Qy        411 GTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTG 470
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Qy        471 GGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGT 530
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Db        441 GGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGT 500

Qy        531 GTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAAT 590
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Db        501 GTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAAT 560

Qy        591 TACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTG 650
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Db        561 TACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTG 620

Qy        651 GACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCG 710
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Db        621 GACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCG 680

Qy        711 CCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCT 770
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Db        681 CCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCT 740

Qy        771 GCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCAT 830
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Db        741 GCCCTGGACTTT-CCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCAT 799

Qy        831 CCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCAC 890
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Db        800 CCTGTGCAGCTGACACACAGCTAAAGAGCCTCATAGCCTGGCGGGGGGCTGGCAGACCCC 859

Qy        891 ACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCA--GGGCACTT 948

Db        860 ACCCCCAGTGCCTGTGCCCAAAGGGCTTCAGTCAGCCGCTCACTCCCTCAAGGGCACCTT 919

Qy        949 TTAGGAAAGGGTTTT------TAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCC 1002

Db        920 TTAGGAAAAGGGTTTTTTACCTAGGGTTTTTTCCTCGCCTTTTTAAGGACCTTCAGCCCC 979

Qy       1003 GCCTGCAGTGG 1013

Db        980 GCCTGCAATGG 990


RESULT 29
BX382425
LOCUS       BX382425               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX382425 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI080YG18 5-PRIME, mRNA sequence.
ACCESSION   BX382425
VERSION     BX382425.1  GI:30439927
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI080BD09QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI080BD09QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="CS0DI080YG18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           56.9%;  Score 860.2;  DB 13;  Length 1201;
  Best Local Similarity  94.3%;  Pred. No. 1.3e-143;
  Matches  931;  Conservative    4;  Mismatches   44;  Indels    8;  Gaps    4;

Qy         22 GGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGG 81

Db         37 GGGATCGGCGGCACGGCGGCGACGGCGACATGGANANCGGGGCCTACGGCGCGGCCAAGG 96

Qy         82 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 141

Db         97 CGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCG 156

Qy        142 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 201

Db        157 TGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATG 216

Qy        202 CCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 261

Db        217 CCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATG 276

Qy        262 GCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT 321

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Db        337 ATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCT 396

Qy        382 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 441

Db        397 TCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGG 456

Qy        442 CAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 501

Db        457 CAGTCACCAACCCGAA-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCT 515

Qy        502 TCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 561

Db        516 TCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACA 575

Qy        562 AGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTG 621

Db        576 AGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTG 635

Qy        622 CCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGA 681

Db        636 CCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGA 695

Qy        682 ACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGG 741

Db        696 ACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGG 755

Qy        742 GAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAC 801

Db        756 GAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAAC 815

Qy        802 TGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCT 861

Db        816 TGCCAGCGCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGSCT 875

Qy        862 CATAGCCTGGC-GGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCA 920

Db        876 CATAGCCTGGCAGGGGGCTGGCAGAGCACACCCCAAGGTGCCTGTTCCCAGAGGGTTTCA 935

Qy        921 GTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCT 980

Db        936 GTAA---SCGCTACTCCTCAGGGGACTTTTAGGAAAGGGTTTT---AGCTAGTTTTTTCT 989

Qy        981 CGCTTTTAATGACCTCAGCCCCGCCTG 1007

Db        990 CGCTTTTAATGACYMGCCCCGCTKCAG 1016


RESULT 30
AL527662
LOCUS       AL527662               1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL527662 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC026YD11 5-PRIME, mRNA sequence.
ACCESSION   AL527662
VERSION     AL527662.2  GI:31065513
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
```

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  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12791155.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC026CB06QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC026CB06QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DC026YD11"
                      /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             56.9%;  Score 859.6;  DB 9;  Length 1201;
  Best Local Similarity   97.4%;  Pred. No. 1.7e-143;
  Matches  910;  Conservative    5;  Mismatches   14;  Indels    5;  Gaps    4;

Qy         53 GGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 112
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Db         61 GGGATGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 120

Qy        113 GACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTC 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTC 180

Qy        173 CTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTT 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTT 240

Qy        233 CAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGC 292
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Db        241 CAACCGCAACGAGGATKCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGC 300

Qy        293 CTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCG 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCG 360

Qy        353 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 412
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Db        361 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 420

Qy        413 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGG 472
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Db        421 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGG 480

Qy        473 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 532
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Db        481 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 540

Qy        533 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 592
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Db        541 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 600

Qy        593 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 652
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Db        601 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 660

Qy        653 CAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCC 712
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Qy        713 CCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 772
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Db        721 CCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 780

Qy        773 CCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 832
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Db        781 CCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 840

Qy        833 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACAC 892
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Db        841 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACAC 899

Qy        893 CCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAG 952
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Db        900 CCCAAGTGCCTGTTCCCAGA-GGSTTCAGTCAGCTGCTCACT-CTCCAGGGCACTTTAAG 957

Qy        953 GAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTT 986
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Db        958 --AAAGGGTTTTAGCTAGTGTTTTYCTCSCTTTW 989


RESULT 31
AL550567
LOCUS       AL550567               1130 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL550567 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI058YI03 5-PRIME, mRNA sequence.
ACCESSION   AL550567
VERSION     AL550567.2  GI:31272384
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1130)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12887656.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI058AE02QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI058AE02QP1.
FEATURES              Location/Qualifiers
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                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             56.7%;  Score 858;  DB 9;  Length 1130;
  Best Local Similarity   95.1%;  Pred. No. 3.3e-143;
  Matches  924;  Conservative    4;  Mismatches   39;  Indels    5;  Gaps    4;

Qy        184 GTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACG 243
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Db         60 GGGATGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACG 119

Qy        244 AGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCT 303
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Db        120 AGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCT 179

Qy        304 TCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGG 363
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Db        180 TCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGG 239

Qy        364 TCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCT 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCT 299

Qy        424 TCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTG 483
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Qy        484 TGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCC 543
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Db        359 TGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCC 418

Qy        544 TGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCA 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCA 478

Qy        604 CTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAAC 663
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Db        479 CTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAAC 538

Qy        664 AGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACT 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 AGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACT 598

Qy        724 GAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTC 783
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTC 658

Qy        784 CCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGA 843
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 CCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGA 718

Qy        844 CACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCT 903
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        719 CACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACACCCCAAGTGCCT 777

Qy        904 GTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTT 963
              ||||||||||: ||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 GTGCCCAGAGGSTTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTT 837

Qy        964 TAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCA 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCA 897

Qy       1024 GCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGT 1083
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        898 GCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTT-CCCCCGGCCCGGGTCAGGC--G 954

Qy       1084 GGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCT 1143
              ||   |||||||||||||||      | |||   | | ||   ::|   |   ||| :
Db        955 TGGGAGCGCTATTATCTGCGTCTCTGCCAAAATCGTGGGGGCATMMACTGCCTGTGCASG 1014

Qy       1144 GTGCAGCGGAGC 1155
              |  | |   |||
Db       1015 GACCGGACMAGC 1026


RESULT 32
BM473487
LOCUS       BM473487                1095 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6484148 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5537979
            5', mRNA sequence.
ACCESSION   BM473487
VERSION     BM473487.1  GI:18522529
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1095)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12230  row: c  column: 04
            High quality sequence stop: 665.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5537979"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             56.7%;  Score 857.6;  DB 12;  Length 1095;
  Best Local Similarity   93.5%;  Pred. No. 3.8e-143;
  Matches  950;  Conservative    0;  Mismatches   59;  Indels    7;  Gaps    5;

Qy        493 CCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACC 552
              |  |  ||||     ||  |  ||  ||  ||  ||||||||||||||||||||||||||
Db          1 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGGGTGTGCTGGCCTCCCTGGCCTACC 60

Qy        553 AGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACC 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACC 120

Qy        613 CCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCT 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCT 180

Qy        673 TCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGG 732
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        181 TCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGG 240

Qy        733 TTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCC 792
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        241 TTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCC 300

Qy        793 TCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCT 852
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Db        301 TCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCT 360

Qy        853 AAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGA 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGA 420

Qy        913 GGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTG 480

Qy        973 TTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCC 1032
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Db        481 TTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCC 540

Qy       1033 CATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGC 1092

Db        541 CATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGC 600

Qy       1093 TATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGG 1152

Db        601 TATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGG 660

Qy       1153 AGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTAT 1212

Db        661 AGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTAT 720

Qy       1213 GATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGC 1272

Db        721 GATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAAGGC 780

Qy       1273 GGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTT 1332

Db        781 GGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCA-CCCGGGCAGCAAGGAAGGGCTTT 839

Qy       1333 GCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGA 1392

Db        840 GCCTGACA--CACCCACTTTATGTAAATATTCTGCAGTTGGTACTTAGAAACCTGGGGGA 897

Qy       1393 GGGCAGGGGTGCCCCAT-GGCTCCCAGACTCT-GTCTGTGCCGAGTGTATTATAAAAT-- 1448

Db        898 AGGCAGGGGTGCCCCATGGGCTCCCAGAATCTGGTCTGGGCCCGATGGATTATAAAATTC 957

Qy       1449 CGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTC 1504

Db        958 GGGGGGGAAAATGCCCGCCCGGGAAATCTGTTTGGGAAACGGAAAAAAGGGTTTTC 1013


RESULT 33
CA488420
LOCUS       CA488420                963 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10809074 MAPcL Homo sapiens cDNA clone IMAGE:6720177 5',
            mRNA sequence.
ACCESSION   CA488420
VERSION     CA488420.1  GI:24950252
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 963)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14279  row: e  column: 09
            High quality sequence stop: 681.
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                     /mol_type="mRNA"
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                     /clone="IMAGE:6720177"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match             56.6%;  Score 855.2;  DB 14;  Length 963;
  Best Local Similarity   95.7%;  Pred. No. 9.9e-143;
  Matches  911;  Conservative    0;  Mismatches   35;  Indels    6;  Gaps    3;

Qy         57 AGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACG 116

Db          1 AGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACG 60

Qy        117 CAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGC 176

Db         61 CAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGC 120

Qy        177 ATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAAC 236

Db        121 ATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAAC 180

Qy        237 CGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCG 296

Db        181 CGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCG 240

Qy        297 GCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAG 356

Db        241 GCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAG 300

Qy        357 TACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGT 416

Db        301 TACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGT 360

Qy        417 TTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCC 476

Db        361 TTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCC 420

Qy        477 GACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTG 536

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Qy        537 GCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTT 596

Db        481 GCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTT 540

Qy        597 GACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAAC 656

Db        541 GACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAAC 600

Qy        657 TACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCT 716

Db        601 TACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCT 660

Qy        717 GTGTACTGAGTGGCGGTTA--GCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCC 774

Db        661 GTGTACTGAGCGGCGGTTAAGCGTGGGAAGGGGGGACAGAGAGGGCCCTCCCCTCTGCCC 720

Qy        775 TGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTG 834

Db        721 TGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTG 780

Qy        835 TGCAGCTGACACACAGCTAAGGAG---CCTCATAGCCTGGCGGGGGGCTGGCAGAGCCACA 891

Db        781 TGCAGCTGACACACAGCTTAAGAGCTCCTTTANCCCGGGCGGGGGGCTGGCAGAGCCACA 840

Qy        892 CCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTA 951

Db        841 CCCCAAGTGCCTGTGCCCANAAGGCTTCAGTCAGCCGCTCACTCCTCAGGCCACTTTTTA 900
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Qy        952 -GGAAAGGGTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCC 1002
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Db        901 GGGAAAGGTTTTAAGCTAAGGTTTTTCCTCGCTTTTAATGAACTCCACCCC 952

RESULT 34
BM458513
LOCUS       BM458513                 1137 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6413953 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497156
            5', mRNA sequence.
ACCESSION   BM458513
VERSION     BM458513.1  GI:18507553
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1137)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12126  row: n  column: 05
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5497156"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_85"
                     /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.867 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            56.5%;  Score 854.6;  DB 12;  Length 1137;
  Best Local Similarity  93.4%;  Pred. No. 1.3e-142;
  Matches  970;  Conservative    0;  Mismatches   55;  Indels   13;  Gaps    7;

Qy         47 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 106
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Db          1 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 60

Qy        107 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 120

Qy        167 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 180

Qy        227 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 240

Qy        287 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 300

Qy        347 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 406
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Db        301 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 360

Qy        407 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 466
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Db        361 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 420

Qy        467 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 526
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Db        421 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 480

Qy        527 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 586
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Db        481 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 540

Qy        587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646
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Qy        647 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 706
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Db        601 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 660

Qy        707 GCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 766
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Db        661 GCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 720

Qy        767 CTCTG-CCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGT 825
              ||||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        721 CTCTGCCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGT 780

Qy        826 TCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC--TGGCGGGGGCTGGCA 883
              ||||||||||||||||||||||||||||||||||||||  ||    |  ||||||||||
Db        781 TCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCCTAACCCTGGCGGGGGGCTGGCA 840

Qy        884 GAGCCACA-CCCCAAGTGCCTGTGCCC--AGAGGGCTTCAGTCAGCCGCTCACTCCTCCA 940
                | ||||| |||||||||||||||||        ||    ||||  ||||||||||||||||
Db        841 AAACCACACCCCCAAGTGCCTGTGCCCCAGAGGGCTTTCANTCAGCCGCTCACTCCTCCA 900

Qy        941 GGGCACTTTTAGGAAAGGG---TTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCA 997
              ||   |  ||||  | ||  ||    ||||        |  |||||  ||||  ||||||||| |||
Db        901 GGCAATTTTTTAGGAAAGGGTTTTTTACCTAGGGGTTTCCCTCCCTTTTAATGAACTCC 960

Qy        998 GCCCCGCCTGCAGTGG---CTAGAAGCCAGCAGGTGCCCATGTGCTAC-TGACAAGTGCC 1053
              |||||   |   ||||      |  | | |     || |||||| |||||  ||||||   | |
Db        961 GCCCCCGCCTGAATGGGGCTAAAAACCAACAAGGGGCCCATGGGCTACTTGACAATGGGC 1020

Qy       1054 TCAGCTTCCCCCCGGCCC 1071
              |||  ||||||||  | ||
Db       1021 TCACTTTCCCCCCCGGCC 1038

RESULT 35
AL555975
LOCUS       AL555975                 1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL555975 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK010YO13 5-PRIME, mRNA sequence.
ACCESSION   AL555975
VERSION     AL555975.2  GI:31277779
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12898221.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
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          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 8916.f For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DK010AH07QP1&cluster=8916.f. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DK010AH07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             56.4%;  Score 852.8;  DB 9;  Length 1201;
  Best Local Similarity   94.9%;  Pred. No. 2.8e-142;
  Matches  911;  Conservative   11;  Mismatches   33;  Indels    5;  Gaps    4;

Qy         38 CGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGA 97
              | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 CCGGGATGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGA 110

Qy         98 CCTGCGGCGCTTCCTGACGCAGCCGCAGGTGG-TGGCGCGCGCCGTGTGCTTGGTCTTCG 156
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        111 CCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGNTGGCGCGCGCCGTGTGCTTGGTCTTCG 170

Qy        157 CCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGC 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGC 230

Qy        217 AGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGG 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 AGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGG 290

Qy        277 TGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCA 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCA 350

Qy        337 GCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGA 396
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        351 GCAACGCCACTGACCGCAARTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGA 410

Qy        397 CCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGA 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 CCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGA 470

Qy        457 AGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCA 516
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 A-GACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCA 529

Qy        517 TCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 TCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACG 589

Qy        577 ACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACC 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        590 ACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTAMC 649

Qy        637 CAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG 709

Qy        697 AGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGA 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 AGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGA 769

Qy        757 GGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCT 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        770 GGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCT 829

Qy        817 TTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGG 876
              |||||||||:|||||||||||||||:|||||||||||| ||||||||||||||||||||
Db        830 TTCACCTGTTSCATCCTGTGCAGCTGAMACACAGCTAAGGAGACTCATAGCCTGGCGGGG 889

Qy        877 GCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCC 936
              |:||| |||: |||||||||||||||||||||||||||| ||||||||:|    :  | |
Db        890 GSTGGGAGAR-CACACCCCAAGTGCCTGTGCCCAGAGGGTTTCAGTCASC--GCTMACTC 946

Qy        937 TCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTC 996
              ||||||||||||||||||||||||||||      : : ||| ||       | | | |:| |
Db        947 TCCAGGGCACTTTTAGGAAAGGGTTTTAGCWARTKTTTTCTCGCTTTAATGACTMASCCC 1006


RESULT 36
BU855955
LOCUS       BU855955                 919 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10453927 NIH_MGC_109 Homo sapiens cDNA clone
            IMAGE:6645546 5', mRNA sequence.
ACCESSION   BU855955
VERSION     BU855955.1  GI:24040921
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2882  row: o  column: 18
            High quality sequence stop: 646.
FEATURES             Location/Qualifiers
     source          1. .919
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6645546"
                     /tissue_type="teratocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_109"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming.  Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G).  Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT*(Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             55.5%;  Score 839;  DB 13;  Length 919;
  Best Local Similarity   97.4%;  Pred. No. 7.7e-140;
  Matches  895;  Conservative    0;  Mismatches   20;  Indels    4;  Gaps    4;

Qy         47 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 60
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Qy        107 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 120

Qy        167 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 180

Qy        227 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 240

Qy        287 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 300

Qy        347 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 406
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Db        301 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 360

Qy        407 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 420

Qy        467 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 480

Qy        527 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 540

Qy        587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 600

Qy        647 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 660

Qy        707 GCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA-GGGGGACAGAGAGGG-CCCTC 764
              |||||||||||||||||||| ||||||||||||||||| ||||||||||||||| |||||
Db        661 GCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGGACAGAGAGGGCCCCTC 720

Qy        765 CCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTG 824
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 CCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTG 780

Qy        825 TTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGC-GGGGGCTGGCA 883
              ||||||||||||||||||||||||||||||||||| |   | || ||| |||||||||||
Db        781 TTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCTTTTAACCCGGGCGGGGGGCTGGCA 840

Qy        884 GAGCCACACCCCAAGTGCCTGTG-CCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGG 942
              || ||||||||| |||||||||| |||| |||||||||||||||||||||||||||  | 
Db        841 GAACCACACCCCCAGTGCCTGTGCCCCAAAGGGCTTCAGTCAGCCGCTCACTCCTCAGGA 900

Qy        943 GCACTTTTAGGAAAGGGTT 961
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Db        901 ACTTTTTAAGAAAAGGTTT 919
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RESULT 37
BX370800

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LOCUS       BX370800                 935 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX370800 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL012YE15 5-PRIME, mRNA sequence.
ACCESSION   BX370800
VERSION     BX370800.1  GI:30453957
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAG061ZF05_CS05798_1&cluster=8916.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAG061ZF05_CS05798_1.
FEATURES             Location/Qualifiers
     source          1..935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL012YE15"
                     /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             55.4%;  Score 838.2;  DB 13;  Length 935;
  Best Local Similarity   95.9%;  Pred. No. 1.1e-139;
  Matches  866;  Conservative    0;  Mismatches   36;  Indels    1;  Gaps    1;

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
              || |  | |  |||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 CCCCCTCCGGACCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 74

Qy        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 134

Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 ACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 194

Qy        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 TTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 254

Qy        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 314

Qy        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 374

Qy        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 434

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 494

Qy       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 554
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Qy       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 614

Qy       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCC 674

Qy       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
               |||||||||||| ||||||||||||||||||||| ||||||||||||||||||||||
Db        675 GTGTGTGAGGGCGNGGCTGGTGCTCATGGCACTTCCTNCTTGCTCCCACCCCTGGCAGCA 734

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db        735 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGNTGNTACTTAN 794

Qy       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
             |||||||||||||||||||||||||||||||  ||||||||||||||||||       |
Db        795 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCNTCCAGACTCTGTCTGTGCCGGTGTATT 854

Qy       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTG-TTTGGAGACGGAATAAATGTT 1499
                |||     |||||||||||||| ||  ||||||| |||||||| ||||||||||
Db        855 ATAAAATCGNGGGGGGAGATGCCCGNCCCTGGATGCTGNTTTGGAGACCGAATAAATGTT 914

Qy       1500 TTC 1502
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Db        915 TTC 917
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RESULT 38
AL572302/c

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LOCUS       AL572302               1035 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL572302 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI007YM24 3-PRIME, mRNA sequence.
ACCESSION   AL572302
VERSION     AL572302.2  GI:31293687
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12930439.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI007BG12NP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI007BG12NP1.
FEATURES             Location/Qualifiers
     source          1. .1035
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                     /clone="CS0DI007YM24"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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Query Match 55.3%; Score 836.4; DB 9; Length 1035;

Best Local Similarity 91.9%; Pred. No. 2.3e-139;
Matches 946; Conservative 15; Mismatches 56; Indels 12; Gaps 8;

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Qy        426 CTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTG 485
              |||||||||||||||| |||||||| |||:|||||::|||| ||||| |   || ||
Db       1019 CTCACCAACCAGTGGG-AGTCACCACCCCSAAGGACKYGCTGTTGGGGCCAMTCTGTGA- 962

Qy        486 AGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTG 545
                |||:|||||||||| |:||||:|||:||||||:||||: |||||||||||: |||||
Db        961 --GGCMGCCATCACCTCCRGCTTSTTTBCCATCTKCTCCKYGGGTGTGCTGGCSCCCCTG 904

Qy        546 GCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACT 605
              ||  |||||||||||||||||||||||||||||||| |||::|||||||||| |||||||||
Db        903 GCTMACCAGCGCTACAAGGCTGGCGTGGACGATTTCWYCCAGAATTACGTCGACCCCACT 844

Qy        606 CCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAG 665
              |||||| |||||||||    |  |  ||||||:|||||||||||||:|||||||||
Db        843 CCGGACGCCAACACTGCTACGCCTCCTATCCCAGGWGCATCTGTGGACAAYTACCAACAG 784

Qy        666 CCACCCTTCACCC-AGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTG 724
              |||||||||||| |||||||||||||||||| ||||||||||||||||||||||||||
Db        783 CCACCCTTCACCCGAGAACGCGGAGACCACCGA-GGCTACCAGCCGCCCCCTGTGTACTG 725

Qy        725 AGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCC 784
              || |||| |      || | |||  | |||  |||| |||| | |||||||| |||||
Db        724 AGCGGCGTTAGCGTGGGAAGGGGACAGAGA---GGCCNTCCCNTTTGCCCTGGANTTTCC 668

Qy        785 CATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGAC 844
              ||| |||||||||||| | ||||||||||||||||||||| ||||||||||||||||||
Db        667 CATGAGCCTCCTGGAANTNCCAGCCCCTCTCTTTCACCTGTNCCATCCTGTGCAGCTGAC 608

Qy        845 ACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTG 904
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 ACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCT-GCAGAGCCACACCCCAAGTGCCTG 549

Qy        905 TGCCCAGAGGGCTTCAGTCAGCCGCTC-ACTCCTCCAGGGCACTTTTAGGAAAGGGTTTT 963
              |||||||||||||||||||||||||| |: ||||||||||||||||||||||||||||||
Db        548 TGCCCAGAGGGCTTCAGTCAGCCGATVGACTCCTCCAGGGCACTTTTAGGAAAGGGTTTT 489

Qy        964 TAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCA 1023
              |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Db        488 TAGCTAGTGTTTTNCCTCGCTTTTAATGACNTCAGCCCCGCCTGCAGTGGCTAGAAGCCA 429

Qy       1024 GCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGT 1083
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Db        428 GCAGGGGCCCATGTGCNACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGT 369

Qy       1084 GGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCT 1143
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Db        368 GGGAGCCGCTATNATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCT 309

Qy       1144 GTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCA 1203
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCA 249

Qy       1204 CTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGG 1263
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGG 189

Qy       1264 TGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGG 1323
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Db        188 TGTGAGGGCGGGGCTGGNGCTCATGGCACTTCCTCCTNGCTCCCACCCCTGGCAGCAGGG 129

Qy       1324 AAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAA 1383
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        128 AAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTNACTTAGGAA 69

Qy       1384 GCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTAT 1443
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCCTGGGGAGGGCA-GGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTAT 10

Qy       1444 AAAATCGTG 1452
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Db          9 AAAATCGTG 1


RESULT 39
BM563844
LOCUS       BM563844               1098 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6560029 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5741930
            5', mRNA sequence.
ACCESSION   BM563844
VERSION     BM563844.1  GI:18811119
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12759  row: e  column: 03
            High quality sequence stop: 677.
FEATURES             Location/Qualifiers
     source          1. .1098
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5741930"
                     /tissue_type="medulla"
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                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27.  Library  is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 013. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             55.3%;  Score 836.4;  DB 12;  Length 1098;
  Best Local Similarity   94.2%;  Pred. No. 2.4e-139;
  Matches  925;  Conservative    0;  Mismatches   46;  Indels   11;  Gaps    5;

Qy         35 CGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTT 94
              | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 CCGGGATGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTT 72

Qy         95 CGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTT 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 CGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTT 132

Qy        155 CGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAA 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAA 192

Qy        215 GCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGG 274
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Db        193 GCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGG 252

Qy        275 GGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGAT 334
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Db        253 GGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGAT 312

Qy        335 CAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTG 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTG 372

Qy        395 GACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCC 432

Qy        455 GAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTC 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTC 492

Qy        515 CATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGA 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 CATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGA 552

Qy        575 CGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTA 612

Qy        635 CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCAC 694
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Db        613 CCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCAC 672

Qy        695 CGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA-GGGGGACAG 753
              |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db        673 CGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGGACAG 732

Qy        754 AGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTC 813
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        733 AGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTC 792

Qy        814 TCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCT--GG 871
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||  |
Db        793 TCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCTTAGCCTTGGC 852

Qy        872 CGGGGGCTGGCAGAGCCA-CACCCCAAGTGCCTGTG--CCCAGAGGGCTTCAGTCAGCCG 928
              |||||||||||| | ||| | ||||||||||||||||  |||  ||  |  | | |||||
Db        853 GGGGGGCTGGCAAAACCACCCCCCCAAGTGCCTGTGCCCCCGAGGGCTTCAATTAAGCCG 912

Qy        929 CTCACTCCTCCAGGGCACTTTTAGGAAAGGG-----TTTTTAGCTAGTGTTTTTCCTCGC 983
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Db        913 CTCACTCCTTCAGGGGACTTTTTAGGAAAAGGGTTTTTTACCCAAGGGTTTTTCCCCCCC 972

Qy        984 TTTTAATGACCTCAGCCCCGCC 1005
              |||||| || || |  ||| ||
Db        973 TTTTAAGGAACTTAAGCCCCCC 994


RESULT 40
BM924646
LOCUS       BM924646               1112 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6653943 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761053
            5', mRNA sequence.
ACCESSION   BM924646
VERSION     BM924646.1  GI:19375025
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1112)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12809  row: a  column: 22
           High quality sequence stop: 692.
FEATURES             Location/Qualifiers
     source          1. .1112
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5761053"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             54.8%;  Score 828.4;  DB 12;  Length 1112;
  Best Local Similarity   93.0%;  Pred. No. 6.4e-138;
  Matches  926;  Conservative    0;  Mismatches   56;  Indels   14;  Gaps    5;

Qy          24 GGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 83
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Db          15 GGGATCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCG 74

Qy          84 GGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 143
               ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          75 GGCGGCTCCTTCGACCTGCGGCGCTTCGTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTG 134

Qy         144 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCC 203
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Db         135 TGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGGTACAGCAATGCC 194

Qy         204 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 263
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Db         195 CACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGC 254

Qy         264 AGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTAT 323
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Db         255 AGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTAT 314

Qy         324 TTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTC 383
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Db         315 TTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTC 374

Qy         384 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCA 443
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         375 TCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCA 434

Qy         444 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 503
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         435 GTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTC 494

Qy         504 AGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 563
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Db         495 AGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAG 554

Qy         564 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 623
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Db         555 GCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCC 614

Qy         624 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 683
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Db         615 TACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAAC 674

Qy         684 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGA 743
               |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         675 GCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGA 734

Qy         744 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTG 803
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Db         735 AGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTG 794

Qy         804 CCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACA-GCTAAGGAGCCTC 862
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Db         795 CCAGCCCCTCTCTTTCACCTGGTCCATCCTGTGCAGCTGACACACAGGCTAAGGAGCCTC 854

Qy         863 ATAGCCTGGCGGGGG---CTGGCAGAGCCACACCCCAAGTGCC-----TGTGCCCAGAGG 914
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Qy         915 GCTTCAGTCAGCCG-CTCACTCCTCCAGGG----CACTTTTAGGAAAGGGTTTTTAGCTA 969
               | |||||||| ||| |||||||||||| ||    |  ||   | || ||||||| |||||
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Qy         970 GTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCC 1005
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RESULT 41
AL542882
LOCUS       AL542882                 920 bp    mRNA    linear   EST 12-MAY-2003
DEFINITION  AL542882 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YD21
            5-PRIME, mRNA sequence.
ACCESSION   AL542882
VERSION     AL542882.2  GI:30548484
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12875358.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8916.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DE013CB11QP1&cluster=8916.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DE013CB11QP1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DE013YD21"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             54.6%;  Score 826;  DB 9;  Length 920;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-137;
  Matches  851;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;
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Qy         53 GGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 112
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Db         65 GGGATGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCT 124

Qy        113 GACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTC 172
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Db        125 GACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTC 184

Qy        173 CTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTT 232
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Qy        233 CAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGC 292
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Qy        293 CTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCG 352
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Qy        353 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 412
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Db        365 CAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGT 424

Qy        413 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGG 472
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        425 TGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAA-GACGTGCTGGTGGG 483

Qy        473 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGT 543

Qy        533 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 592
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Db        544 GCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTA 603

Qy        593 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 652
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Db        604 CGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGA 663

Qy        653 CAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCC 712
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Qy        713 CCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 772
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        724 CCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGC 783

Qy        773 CCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 832
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        784 CCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCC 843

Qy        833 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACAC 892
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        844 TGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG-CACAC 902

Qy        893 CCCAAGTGCCTGTGCCCA 910
              ||||||||||||||||||
Db        903 CCCAAGTGCCTGTGCCCA 920
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RESULT 42
BM914997
LOCUS       BM914997               1076 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6702297 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481121
            5', mRNA sequence.
ACCESSION   BM914997
VERSION     BM914997.1  GI:19365376
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1076)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2005  row: b  column: 02
            High quality sequence start: 10
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5481121"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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  Query Match             54.5%;  Score 823.6;  DB 12;  Length 1076;
  Best Local Similarity   94.6%;  Pred. No. 4.6e-137;
  Matches  897;  Conservative    0;  Mismatches   41;  Indels   10;  Gaps    4;

Qy         27 GGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGC 86
              ||  ||||    || ||| |||||  ||||||||||||||||||||||||||||||||||
Db          1 GGTGGCAATTCCGACGAGGGCGA-ATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGC 59

Qy         87 GGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGC 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 GGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGC 119

Qy        147 TTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCAC 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCAC 179

Qy        207 GAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGT 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGT 239

Qy        267 GCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCTTCTTCTTGGTGGTCGACGCGTATTTC 326
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        240 GCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCTTTCTTCTTGGTGGTCGACGCGTATTTC 299

Qy        327 CCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCA 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCA 359

Qy        387 GCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTC 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTC 419

Qy        447 ACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGC 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGC 479

Qy        507 TTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCT 566
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Db        480 TTCTTTTCCATCTTCTCCTGNGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCT 539

Qy        567 GGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTAC 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTAC 599

Qy        627 GCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCG 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCG 659

Qy        687 GAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGG 746
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db        660 GAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGGAGG 719

Qy        747 GGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA 806
              |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        720 GGGACAGAGAAGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCA 779

Qy        807 GCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAG 866
              |||||||||||||||||||||||||||||||||||||||||||||||||||       |
Db        780 GCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCTCNTAAA 839

Qy        867 CCTGG---CGGGGGCTGGCAGAGCCACACCCCAAGTGCCT---GTGCCCAGAGGGCTTCA 920
              ||  |     |||| |   |   | |||| |||| ||||||    |  ||   |||| ||||
Db        840 CCCTGGCCGGGGGCCGTGGCAAACCACCCCCCAGTGCCTTGGGGCCCAGAAGGGTTTCA 899

Qy        921 GTCAGCCGCTCACTCCTCCAGGGCAC---TTTTAGGAAAGGGTTTTTA 965
              |||||||||||||||  || |||||     |||| ||||||||||||||
Db        900 GTCAGCCGCTCACTCCCTCAAGGCACTTTTTTTGGGAAAGGGTTTTTA 947
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RESULT 43
BU541270
LOCUS       BU541270                 894 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10327418 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6572922
            5', mRNA sequence.
ACCESSION   BU541270
VERSION     BU541270.1  GI:22851711
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2765  row: m  column: 18
            High quality sequence stop: 676.
FEATURES             Location/Qualifiers
     source          1..894
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6572922"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             54.3%;  Score 821;  DB 13;  Length 894;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-136;
  Matches  862;  Conservative    0;  Mismatches   16;  Indels    5;  Gaps    3;
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Qy         32 CAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTC 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTC 60

Qy         92 CTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGT 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGT 120

Qy        152 CTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTC 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTC 180

Qy        212 TAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCAT 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCAT 240

Qy        272 CGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCA 331
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Db        241 CGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCA 300

Qy        332 GATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCT 360

Qy        392 CTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAA 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAA 420

Qy        452 CCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTT 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTT 480

Qy        512 TTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGT 571
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Db        481 TTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGT 540

Qy        572 GGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTC 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTC 600

Qy        632 CTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGAC 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGAC 660

Qy        692 CACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGAC 751
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        661 CACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGAC 720

Qy        752 AGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTG-CCAGCCC 810
              |||||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||
Db        721 AGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGNNCAGCCC 780

Qy        811 CTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC-- 868
              ||||||||||||||||||||||||||||||||||||||||| | |||||||||   |
Db        781 CTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTTAAGAGCCTCATANNCCT 840

Qy        869 TGGCGGGGGCTGGCAGAGCC--ACACCCCAAGTGCCTGTGCCC 909
               | |||||||||| | ||      ||| |||||||||| ||
Db        841 GGNCGGGGGCTGGCANAACCCACACCCCAAAGTGCCTGTGNCC 883
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RESULT 44
BM925611
LOCUS       BM925611                1027 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6710123 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5763820
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            5', mRNA sequence.
ACCESSION   BM925611
VERSION     BM925611.1  GI:19375990
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12816  row: e  column: 05
            High quality sequence start: 26
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5763820"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is  destroyed
                     upon cloning).  Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
ORIGIN
```

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  Query Match             54.1%;  Score 817.6;  DB 12;  Length 1027;
  Best Local Similarity   95.9%;  Pred. No. 5.3e-136;
  Matches  894;  Conservative    0;  Mismatches   29;  Indels    9;  Gaps    5;

Qy         62 GGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCC 121
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 GCCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCC 94

Qy        122 GCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTA 154

Qy        182 TGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAA 241
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Db        155 TGGTGAGGGGTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAA 214

Qy        242 CGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTT 301
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Db        215 CGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTT 274

Qy        302 CTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCT 361
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Db        275 CTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCT 334

Qy        362 GGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTG 421
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Db        335 GGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTG 394

Qy        422 CTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTC 481
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Db        395 CTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTC 454

Qy        482 TGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTC 541
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Db        455 TGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTC 514

Qy        542 CCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCC 574

Qy        602 CACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCA 661
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Db        575 CACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCA 634

Qy        662 ACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTA 721
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Db        635 ACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTA 694

Qy        722 CTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTT 781
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Qy        782 TCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCT 841
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 TCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCT 814

Qy        842 GACACACAGCTAAGGAGCCT-CATAGCCTGGCGGGGG--CTGGCAGAGCCACACCCCAAG 898
              |||||||||||||||||| |||| |||||||||||    | ||||||||||||||||||
Db        815 GACACACAGCTAAGGAGCCTCCATACCCTGGCGGGGGGCTGGCCAGAGCCACACCCCAAG 874

Qy        899 TGCC---TGTGCCCAGAGGGCTTCAGTCAGCC-GCTCACTCCTCCAGGGCAC--TTTTAG 952
              ||||   ||  ||    || |||||||||||| |||||||||| ||||||||  |||||
Db        875 TGCCCTGTGCCCCAGAGGGCCTTCAGTCAGCCGGCTCACTCCTTCAGGGCACTTTTTTAA 934

Qy        953 GAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCT 984
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Db        935 GAAAGGGTTTTTTAGCCTAGGGTTTTTTCCCT 966
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RESULT 45
BQ055557
LOCUS       BQ055557                978 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6838359 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5807747
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ACCESSION   BQ055557
VERSION     BQ055557.1  GI:19814897
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 978)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2050  row: k  column: 12
            High quality sequence stop: 652.
FEATURES             Location/Qualifiers
     source          1. .978
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5807747"
                     /tissue_type="lymphoma, cell line"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 54.1%; Score 817.4; DB 13; Length 978;
Best Local Similarity 96.4%; Pred. No. 5.7e-136;
Matches 836; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Qy         47 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 106
Db          1 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 60

Qy        107 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 166
Db         61 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 120

Qy        167 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 226
Db        121 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 180

Qy        227 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 286
Db        181 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 240

Qy        287 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 346
Db        241 CCTGGCCTCGGCTTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 300

Qy        347 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 406
Db        301 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 360

Qy        407 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 466
Db        361 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 420

Qy        467 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 526
Db        421 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 480

Qy        527 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 586
Db        481 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 540

Qy        587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646
Db        541 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 600

Qy        647 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 706
Db        601 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 660

Qy        707 GCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 766
Db        661 GCCGCCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 720

Qy        767 CTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTT 826
Db        721 CTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTT 780

Qy        827 CCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGGCTGGCAGAG 886
Db        781 CCATCCTGTGCAGCTGACACACAGCTAAAGAGGCTCATAACCCTGGCGGGGGGGCTGGCC 840
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Qy        887 CCACACCCCAAGTGCCTGTGCCCAGAG 913
Db        841 AAAGCCCACACCCCCAAGTGCCTTGTG 867
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RESULT 46
BU542737
LOCUS BU542737 861 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10334568 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574660 5', mRNA sequence.
ACCESSION BU542737
VERSION BU542737.1 GI:22853220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 861)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2770 row: f column: 04
High quality sequence stop: 696.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6574660"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 54.0%; Score 816.4; DB 13; Length 861;
Best Local Similarity 97.0%; Pred. No. 8.3e-136;
Matches 832; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy         54 GAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTG 113
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Qy        114 ACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCC 173
Db         61 ACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCC 120

Qy        174 TGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTC 233
Db        121 TGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTC 180

Qy        234 AACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCC 293
Db        181 AACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCC 240

Qy'       294 TCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGC 353
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Db        241 TCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGC 300

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Db        301 AAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTT 360

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Qy        474 GCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTG 533
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Db        421 GCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTG 480

Qy        534 CTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTAC 593
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Db        481 CTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTAC 540

Qy        594 GTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGAC 653
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Db        541 GTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGAC 600

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Db        601 AACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCC 660

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Qy        774 CTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCT 833
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Db        721 CTGGACTTTTCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCT 780

Qy        834 GTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACC 893
              |||||||||||||||||||| |||||||||  |    | |||  ||| | ||   | ||
Db        781 GTGCAGCTGACACACAGCTAAAGAGCCTCATAAACCTTGGCGGGGGGGCTGGGCAGAAGC 840

Qy        894 CCAAGTGCCTGTGCCCAG 911
              |  |   || ||||| |
Db        841 CACACCCCCAGTGCCCTG 858


RESULT 47
BU541667
LOCUS       BU541667                910 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10333661 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573382
            5', mRNA sequence.
ACCESSION   BU541667
VERSION     BU541667.1  GI:22852108
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2766  row: p  column: 22
            High quality sequence stop: 658.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6573382"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             53.8%;  Score 814.2;  DB 13;  Length 910;
  Best Local Similarity   98.4%;  Pred. No. 2.1e-135;
  Matches  853;  Conservative    0;  Mismatches   10;  Indels    4;  Gaps    3;

Qy         47 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 106
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Db          1 CGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCG 60

Qy        107 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 166
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Db         61 CTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGT 120

Qy        167 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 226
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Db        121 GTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTG 180

Qy        227 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 286
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Db        181 CGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTT 240

Qy        287 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 346
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Db        241 CCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCAC 300

Qy        347 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 406
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Db        301 TGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTG 360

Qy        407 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCT 420

Qy        467 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 526
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Db        421 GGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTG 480

Qy        527 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCA 540

Qy        587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 600

Qy        647 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCA 706
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Db        601 TGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGANGGCTACCA 660

Qy        707 GCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 766
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Db        661 GCCGCCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 720

Qy        767 CTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTT 826
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Db        721 CTCTGGCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCCGCCCCTCTCTTTCACCTGTT 780

Qy        827 CCATCCTGTGCAGCTGACACACAG-CTAAGGAGCCTCATAGCCTGGCGGGGG--CTGGCA 883
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Db        781 CCATCCTGTGCAGCTGACACACAGCCTAAAGAGCCTCATAGCCTGGCGGGGGGCCTGGCA 840

Qy        884 GAGCCACA-CCCCAAGTGCCTGTGCCC 909
                 | || ||  ||||||||||||| ||||
Db        841 NAACCCCACCCCCAAGTGCCTGGGCCC 867


RESULT 48
BI821013
LOCUS       BI821013                891 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603035668F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176745 5',
            mRNA sequence.
ACCESSION   BI821013
VERSION     BI821013.1  GI:15932563
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 891)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11440  row: g  column: 18
            High quality sequence stop: 828.
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                     /clone="IMAGE:5176745"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            53.7%;  Score 811.4;  DB 12;  Length 891;
  Best Local Similarity  98.6%;  Pred. No. 6.6e-135;
  Matches  829;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy         43 ACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGC 102
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Db          1 ACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGC 60

Qy        103 GGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGA 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGA 120

Qy        163 TCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGT 222
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Db        121 TCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGT 180

Qy        223 ACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGG 282
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Db        181 ACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGG 240

Qy        283 CCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACG 342
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Db        241 CCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACG 300

Qy        343 CCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCC 402
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Qy        403 TGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACG 462
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Db        361 TGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACG 420

Qy        463 TGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCT 522
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Db        421 TGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCT 480

Qy        523 CCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCA 582
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Db        481 CCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCA 540

Qy        583 TCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTG 642
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Db        541 TCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTG 600

Qy        643 CATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCT 702
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Db        601 CATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCT 660

Qy        703 ACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAG-AGAGGGCC 761
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Qy        822 CTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGG 881
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Db        781 CTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGAGCTGA 840

Qy        882 C 882
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Db        841 C 841


RESULT 49
BQ066331
LOCUS       BQ066331                976 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6861020 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5930967
            5', mRNA sequence.
ACCESSION   BQ066331
VERSION     BQ066331.1  GI:19895377
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 976)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2111  row: i  column: 16
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                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

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ACCESSION   BU539619
VERSION     BU539619.1  GI:22850060
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2759  row: d  column: 18
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                     following 5' adaptor: GGCACGAG(G).  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             53.5%;  Score 809.4;  DB 13;  Length 882;
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GenCore version 5.1.6

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Run on: April 8, 2004, 11:04:56 ; Search time 553 Seconds
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Searched: 2475585 seqs, 1875730760 residues

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SUMMARIES

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ALIGNMENTS

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; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 1512; DB 9; Length 1512;
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
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Db       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

Qy       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
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Qy       1501 TCTCATTCAAAG 1512
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Db       1501 TCTCATTCAAAG 1512
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RESULT 3
US-09-978-192A-161
; Sequence 161, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 100.0%; Pred. No. 0;
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Qy          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
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Db         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
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Db        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180

Qy        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
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Db        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
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Db        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

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Db        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
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Db        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
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Db        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 1512; DB 9; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
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; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1512; DB 10; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
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Qy        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
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Db        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140

Qy       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200

Qy       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

Qy       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380

Qy       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

Qy       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500

Qy       1501 TCTCATTCAAAG 1512
              ||||||||||||
Db       1501 TCTCATTCAAAG 1512
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RESULT 6
US-09-978-608A-161
; Sequence 161, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 161
;   LENGTH: 1512
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-608A-161

  Query Match           100.0%;  Score 1512;  DB 10;  Length 1512;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1512;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60

Qy         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180

Qy        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

Qy        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360

Qy        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420

Qy        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480

Qy        481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
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Qy        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660

Qy        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780

Qy        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840

Qy        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

Qy        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140

Qy       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200

Qy       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

Qy       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380

Qy       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

Qy       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500

Qy       1501 TCTCATTCAAAG 1512
              ||||||||||||
Db       1501 TCTCATTCAAAG 1512
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RESULT 7
US-09-978-585A-161
; Sequence 161, Application US/09978585A

; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 161
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-161

Query Match 100.0%; Score 1512; DB 10; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60

Qy          61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy         121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180

Qy         181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy         241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

Qy         301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360

Qy         361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
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Qy       421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480
Db       421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480

Qy       481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
Db       481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540

Qy       541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600
Db       541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy       601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
Db       601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660

Qy       661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
Db       661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy       721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCCTCTGCCCTGGACT 780
Db       721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCCTCTGCCCTGGACT 780

Qy       781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
Db       781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840

Qy       841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
Db       841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

Qy       901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
Db       901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy       961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
Db       961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy      1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
Db      1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy      1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
Db      1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140

Qy      1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
Db      1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200

Qy      1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
Db      1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

Qy      1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
Db      1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy      1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
Db      1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380

Qy      1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
Db      1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

Qy      1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
Db      1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500

Qy      1501 TCTCATTCAAAG 1512
Db      1501 TCTCATTCAAAG 1512
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RESULT 8
US-09-978-191A-161
; Sequence 161, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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Qy       181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
Db       181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy       241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
Db       241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

Qy       301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
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Qy       361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
Db       361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420

Qy       421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480
Db       421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480

Qy       481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
Db       481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540

Qy       541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600
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Qy       601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
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Qy       661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
Db       661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy       721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
Db       721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780

Qy       781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
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Qy       841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
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Qy       901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
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Qy       961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
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Db      1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy      1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
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Qy      1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
Db      1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

Qy      1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
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Qy      1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
Db      1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380

Qy      1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
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Qy      1441 TATAAAATCGTGGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
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Qy      1501 TCTCATTCAAAG 1512
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Qy         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120
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Db         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
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Qy        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
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Db        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
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Qy        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
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Db        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420

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Db        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
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Db        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
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Qy        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
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Db        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
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Db        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
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Db       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140

Qy       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
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Db       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200

Qy       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
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Db       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

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Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
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Db       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380

Qy       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440
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Db       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

Qy       1441 TATAAAATCGTGGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
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Db       1441 TATAAAATCGTGGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500

Qy       1501 TCTCATTCAAAG 1512
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Db       1501 TCTCATTCAAAG 1512


RESULT 10
US-09-978-564A-161
; Sequence 161, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;  PRIOR APPLICATION NUMBER: 60/085573
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

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  Matches 1512;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60

Qy         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180

Qy        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
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Db        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
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Db        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

Qy        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
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Db        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360

Qy        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
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Db        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420

Qy        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480
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Db        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480

Qy        481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
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Db        481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540

Qy        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
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Db        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660

Qy        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
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Db        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720

Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780

Qy        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840

Qy        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
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Db        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

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Db        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
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Db        961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
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Db       1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
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Db       1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140

Qy       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200
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Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
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RESULT 11
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; Sequence 161, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 1512; DB 10; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
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;  APPLICANT:  Gerber, Hanspeter
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;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C12
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;  CURRENT FILING DATE:  2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1512; DB 10; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
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Qy     661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
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Qy     781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
Db     781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840

Qy     841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900
Db     841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

Qy     901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960
Db     901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

Qy     961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020
Db     961 TTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAG 1020

Qy    1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080
Db    1021 CCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGC 1080

Qy    1081 CGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGC 1140
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Db       1141 CCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGC 1200

Qy       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCG 1260

Qy       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320
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Db       1261 TGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCA 1320

Qy       1321 GGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAG 1380
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Db       1381 GAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTAT 1440

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Qy       1501 TCTCATTCAAAG 1512
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RESULT 13
US-09-978-824-161
; Sequence 161, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C14
;  CURRENT APPLICATION NUMBER: US/09/978,824
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
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;  PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1512; DB 10; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCG 60
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Qy         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120
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Db         61 GGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGC 120

Qy        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180
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Db        121 CGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCT 180

Qy        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240
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Db        181 ATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCA 240

Qy        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300
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Db        241 ACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCT 300

Qy        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACC 360

Qy        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420
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Db        361 TGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCT 420

Qy        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480
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Db        421 GCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACT 480

Qy        481 CTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCT 540
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Db        541 CCCTGGCCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACC 600

Qy        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660
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Db        601 CCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACC 660

Qy        661 AACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGT 720
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Qy        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780
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Db        721 ACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACT 780

Qy        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840
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Db        781 TTCCCATCAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGC 840

Qy        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

Db        841 TGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTG 900

Qy        901 CCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGT 960

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Qy       1501 TCTCATTCAAAG 1512

Db       1501 TCTCATTCAAAG 1512


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; Sequence 161, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C1
;  CURRENT APPLICATION NUMBER: US/09/918,585A
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C21
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Search completed: April 8, 2004, 14:05:52
Job time : 562 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 8, 2004, 08:56:20 ; Search time 5849 Seconds
(without alignments)
11204.423 Million cell updates/sec

Title: US-10-020-445A-161
Perfect score: 1512
Sequence: 1 cggacgcgtgggcggacgcg.....aaatgttttctcattcaaag 1512

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 10

Total number of hits satisfying chosen parameters: 3107191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1364	90.2	1478	9	BC029755	BC029755 Homo sapi
4	1333	88.2	1491	6	AX779861	AX779861 Sequence
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7	883	58.4	3052	9	HSM804321	AL833010 Homo sapi
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c 9	881	58.3	209751	9	AC087645	AC087645 Homo sapi
10	879	58.1	1254	6	BD189955	BD189955 Tumor ant
11	732	48.4	969	6	AR069079	AR069079 Sequence
12	633	41.9	1977	6	AR184139	AR184139 Sequence
13	633	41.9	1977	6	BD192668	BD192668 123 human
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15	481	31.8	154840	2	AC032035	AC032035 Homo sapi
16	388	25.7	388	6	AX777912	AX777912 Sequence
17	337	22.3	396	6	AR391312	AR391312 Sequence
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37	80	5.3	134	6	AR426936	AR426936 Sequence
38	80	5.3	134	6	BD122489	BD122489 EST and e
39	80	5.3	137	6	AR426937	AR426937 Sequence
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ALIGNMENTS

RESULT 1
AX538190
LOCUS AX538190 1512 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 161 from Patent EP1241184.
ACCESSION AX538190
VERSION AX538190.1 GI:25270341
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
TITLE Human synaptogyrin-like protein and nucleic acids encoding the same
JOURNAL Patent: EP 1241184-A 161 18-SEP-2002;

Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1512
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ORIGIN

Query Match 100.0%; Score 1512; DB 6; Length 1512;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AY358916
VERSION AY358916.1 GI:37182949
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 1512)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1512)
AUTHORS Clark,H.F.

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  TITLE     Direct Submission
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            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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Qy       1441 TATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTT 1500
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Qy       1501 TCTCATTCAAAG 1512
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Db       1501 TCTCATTCAAAG 1512


RESULT 3
BC029755
LOCUS       BC029755                1478 bp    mRNA    linear   PRI 04-OCT-2003
DEFINITION  Homo sapiens synaptogyrin 2, mRNA (cDNA clone MGC:21859
            IMAGE:4341106), complete cds.
ACCESSION   BC029755
VERSION     BC029755.1  GI:20987256
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1 (bases 1 to 1478)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1478)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 26 Row: i Column: 23.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 90.2%; Score 1364; DB 9; Length 1478;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     166 TGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACT 225
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RESULT 4
AX779861
LOCUS       AX779861               1491 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 2018 from Patent WO03039443.
ACCESSION   AX779861
VERSION     AX779861.1  GI:32696855
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE     Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 2018 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ;
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   99.8%;  Pred. No. 0;
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RESULT 5
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LOCUS       HSAJ2308               1491 bp    mRNA    linear   PRI 03-MAR-1998
DEFINITION  Homo sapiens mRNA for synaptogyrin 2.
ACCESSION   AJ002308
VERSION     AJ002308.1  GI:2959871
KEYWORDS    synaptogyrin 2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Kedra,D., Pan,H.Q., Seroussi,E., Fransson,I., Guilbaud,C.,
            Collins,J.E., Dunham,I., Blennow,E., Roe,B.A., Piehl,F. and
            Dumanski,J.P.
  TITLE     Characterization of the human synaptogyrin gene family
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1491)
  AUTHORS   Kedra,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1997) Kedra D., Dept. of Molecular Medicine,
            Clinical Genetics Unit, Karolinska Hospital, CMM building L-8,,
            S-17176 Stockholm, SWEDEN
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ORIGIN
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Query Match 88.2%; Score 1333; DB 9; Length 1491;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1483; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 6
BC000407
LOCUS       BC000407                1708 bp    mRNA    linear   PRI 06-NOV-2003
DEFINITION  Homo sapiens synaptogyrin 2, mRNA (cDNA clone MGC:8571
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ACCESSION   BC000407
VERSION     BC000407.2  GI:38197476
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1708)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
    TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1708)
  AUTHORS   Strausberg,R.
    TITLE   Direct Submission
  JOURNAL   Submitted (15-NOV-2000) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Nov 6, 2003 this sequence version replaced gi:12653276.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 1 Row: k Column: 10
            This clone was selected for full length sequencing because it
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ORIGIN

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Matches 1465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     642 GCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGC 701
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RESULT 7
HSM804321
LOCUS HSM804321 3052 bp mRNA linear PRI 10-JUL-2002
DEFINITION Homo sapiens mRNA; cDNA DKFZp666M214 (from clone DKFZp666M214).
ACCESSION AL833010
VERSION AL833010.1 GI:21733599
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3052)
AUTHORS Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp666M214) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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ORIGIN

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Qy        707 GCCGCCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCC 766
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RESULT 8
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DEFINITION  Homo sapiens chromosome 17, clone RP11-153A23, complete sequence.
ACCESSION   AC021593
VERSION     AC021593.15  GI:22038664
KEYWORDS    HTG.
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REFERENCE   1  (bases 1 to 177738)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-153A23
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 177738)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
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            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 177738)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
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            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 177738)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Aug 1, 2002 this sequence version replaced gi:21702950.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
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VERSION     AC087645.19  GI:27311503
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 209751)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-219G17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 209751)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
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            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 209751)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
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            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 209751)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
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            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
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            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-2003) Whitehead Institute/MIT Center for Genome
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            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Dec 20, 2002 this sequence version replaced gi:26190573.
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            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
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Qy       587 GAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATC 646
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Qy       827 CCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAG 886
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Qy        947 TTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCT 1006
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Qy       1367 CAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC 1426
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VERSION     BD189955.1  GI:32999694
KEYWORDS    WO 03008450-A/65.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1254)
  AUTHORS   Ito,K. and Shichijo,S.
  TITLE     Tumor antigen
  JOURNAL   Patent: WO 03008450-A 65 30-JAN-2003;
            KYOGO ITO,SHIGEKI SHICHIJO
COMMENT     OS   Homo sapiens (human)
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            PD   30-JAN-2003
            PF   11-JUN-2002 WO 2002JP005799
            PR   12-JUN-2001 JP 01P   177058,21-AUG-2001 JP 01P   250728 PI
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            PC   C07K14/705,A61K38/08,C12N15/12,A61K38/17,A61P35/00,C12P21/02,
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Qy        591 TACGTTGACCCCACTCCGGACCCCAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTG 650
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Qy        651 GACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCG 710
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Qy        891 ACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTT 950
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RESULT 11
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ACCESSION   AR069079
VERSION     AR069079.1  GI:6001286
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Hawkins,P.R., Stuart,S.G. and Murry,L.E.
  TITLE     Synaptogyrin homolog
  JOURNAL   Patent: US 5854413-A 1 29-DEC-1998;
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Qy        386 AGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGT 445
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Qy        506 CTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGC 565
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Db        565 CTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGC 624

Qy        566 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 625
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Db        625 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 684

Qy        626 CGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGC 685
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Db        685 CGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGC 744

Qy        686 GGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAG 745
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Qy        746 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCC 805
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Db        805 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCC 864

Qy        806 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 865
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Db        865 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 924

Qy        866 GCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCA 910
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RESULT 12
AR184139
LOCUS       AR184139                1977 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 83 from patent US 6342581.
ACCESSION   AR184139
VERSION     AR184139.1  GI:20228108
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1977)
  AUTHORS   Rosen,C.A., Ruben,S.M., Olsen,H.S. and Ebner,R.
  TITLE     Secreted protein HLHFP03
  JOURNAL   Patent: US 6342581-A 83 29-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .1977
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ORIGIN

  Query Match           41.9%;  Score 633;  DB 6;  Length 1977;
  Best Local Similarity   99.5%;  Pred. No. 3.9e-290;
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Qy        554 GCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCC 613
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Qy        614 CAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTT 673
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Qy        674 CACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGT 733
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Db       1077 CACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGT 1136

Qy        734 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCT 793
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Db       1137 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCT 1196

Qy        794 CCTGGAACTGCCAGCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTA 853
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Qy        854 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 913
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Db       1257 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 1316

Qy        914 GGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 973
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Db       1317 GGNTTCAGTCAGCYGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 1376

Qy        974 TTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCC 1033
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Db       1557 GCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATG 1616

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Db       1856 GGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTCATTCAAA 1913
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RESULT 13
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LOCUS       BD192668                1977 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  123 human secreted proteins.
ACCESSION   BD192668
VERSION     BD192668.1  GI:33002407
KEYWORDS    JP 2002513295-A/82.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1977)
  AUTHORS   Fischer,C.L., Rosen,C.A., Soppet,D.R., Ruben,S.M., Kyaw,H., Li,Y.,
            Zeng,Z., Lafleur,D.W., Moore,P.A., Shi,Y., Ols,H.S., Ebner,R. and
            Brewer,L.A.
  TITLE     123 human secreted proteins
  JOURNAL   Patent: JP 2002513295-A 82 08-MAY-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002513295-A/82
            PD   08-MAY-2002
            PF   07-JUL-1998 JP 1999508744
            PR   08-JUL-1997 US    60/051926,08-JUL-1997 US    60/051929 PR
            08-JUL-1997 US    60/052793,08-JUL-1997 US    60/051925 PR
            08-JUL-1997 US    60/051931,08-JUL-1997 US    60/051932 PR
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            18-AUG-1997 US    60/055948,18-AUG-1997 US    60/055722 PR
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            18-AUG-1997 US    60/055950,18-AUG-1997 US    60/055953 PR
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            L FISCHER,CRAIG A ROSEN,DANIEL R SOPPET,STEVEN M RUBEN, PI   HLA
            KYAW,
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              HENRIK S OLSEN,
            PI   REINHARD EBNER,LAURIE A BREWER
            PC   C07H21/04,C12N15/63
            CC   n equals a,t,g, or c
            CC   n equals a,t,g, or c
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ORIGIN

  Query Match             41.9%;  Score 633;  DB 6;  Length 1977;
  Best Local Similarity   99.5%;  Pred. No. 3.9e-290;
  Matches  953;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy        554 GCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCC 613

Db        957 GCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCC 1016

Qy        614 CAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTT 673

Db       1017 CAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTT 1076

Qy        674 CACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGT 733

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Qy        734 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCT 793

Db       1137 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCT 1196

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Qy        854 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 913

Db       1257 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 1316

Qy        914 GGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 973

Db       1317 GGNTTCAGTCAGCYGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 1376

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Qy       1034 ATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCT 1093

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Qy       1094 ATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGA 1153

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Qy       1154 GCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATG 1213

Db       1557 GCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATG 1616

Qy       1214 ATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCG 1273

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DEFINITION Homo sapiens chromosome 17 clone RP11-219G17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC010532
VERSION AC010532.2 GI:6758797
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 229426)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 17
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 229426)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jan 26, 2000 this sequence version replaced gi:5882406.
-------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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* NOTE: This record contains 99 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Db     110891 GCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCC 110832

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Qy       1427 TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGA 1486
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            IN PROGRESS ***, 18 unordered pieces.
ACCESSION   AC032035
VERSION     AC032035.3  GI:9994161
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 154840)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-141D15
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 154840)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
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            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
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            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Sep 8, 2000 this sequence version replaced gi:7705196.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L9138
                Center clone name: 141_D_15
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 18 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2373: contig of 2373 bp in length
            *     2374     2473: gap of 100 bp
            *     2474     4930: contig of 2457 bp in length
            *     4931     5030: gap of 100 bp
            *     5031     7215: contig of 2185 bp in length
            *     7216     7315: gap of 100 bp
            *     7316     9541: contig of 2226 bp in length
            *     9542     9641: gap of 100 bp
            *     9642    12211: contig of 2570 bp in length
            *    12212    12311: gap of 100 bp
            *    12312    14923: contig of 2612 bp in length
            *    14924    15023: gap of 100 bp
            *    15024    19094: contig of 4071 bp in length
            *    19095    19194: gap of 100 bp
            *    19195    22286: contig of 3092 bp in length
            *    22287    22386: gap of 100 bp
            *    22387    26147: contig of 3761 bp in length
            *    26148    26247: gap of 100 bp
            *    26248    31933: contig of 5686 bp in length
            *    31934    32033: gap of 100 bp
            *    32034    37339: contig of 5306 bp in length
            *    37340    37439: gap of 100 bp
            *    37440    42858: contig of 5419 bp in length
            *    42859    42958: gap of 100 bp
            *    42959    48810: contig of 5852 bp in length
            *    48811    48910: gap of 100 bp
            *    48911    56029: contig of 7119 bp in length
            *    56030    56129: gap of 100 bp
            *    56130    62189: contig of 6060 bp in length
            *    62190    62289: gap of 100 bp
            *    62290    82959: contig of 20670 bp in length
            *    82960    83059: gap of 100 bp
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ORIGIN

  Query Match             31.8%;  Score 481;  DB 2;  Length 154840;
  Best Local Similarity   99.7%;  Pred. No. 3.4e-218;
  Matches  721;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

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Db      92295 AGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACAC 92354

Qy        849 AGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCC 908
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Qy        909 CAGAGGGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCT 968
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Qy        969 AGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAA-GCCAGCAG 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      92475 AGTGTTTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAG 92534

Qy       1028 GTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGA 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1088 GCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGC 1147
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Qy       1148 AGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGC 1207
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Qy       1208 TGTATGATCTGGGGGCCACCACCCT-GTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGT 1266
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Qy       1267 GAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAG 1326
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Qy       1327 GGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCC 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92835 GGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCC 92894

Qy       1387 TGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAA 1446
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Db      92895 TGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAA 92954

Qy       1447 ATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTCAT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1507 TCA 1509
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Job time : 5857 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-10-020-445A-162
Perfect score: 1191
Sequence: 1 MESGAYGAAKAGGSFDLRRF.....QPPFTQNAETTEGYQPPPVY 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	136	11.4	24	4	US-09-227-357-509	Sequence 509, App
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6	93	7.8	18	4	US-09-227-357-510	Sequence 510, App
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ALIGNMENTS

RESULT 1
US-08-700-637-2
; Sequence 2, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT05
; CLONE: 775426
US-08-700-637-2

Query Match 99.5%; Score 1185; DB 2; Length 224;
Best Local Similarity 99.6%; Pred. No. 3.3e-125;
Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        121 VGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQN 180
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RESULT 2
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; Sequence 3, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  231 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  GI 1072118
US-08-700-637-3

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Qy         61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWF 120
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Qy        121 VGFCFLTNQWAVTNPKD--VLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDD-- 176
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Db        178 FCQDYMDPSQDSSMPYAPYVEPSAGSDPTGMGGTYQHPANAFDAE-PQGYQ 227


RESULT 3
US-09-227-357-512
; Sequence 512, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
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;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
```

; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 512
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-512

Query Match 12.4%; Score 148; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 SALWTFLWFVGFCFLTNQWAVTNPK 136
||||||||||||||||||||||||||
Db 1 SALWTFLWFVGFCFLTNQWAVTNPK 25

RESULT 4
US-09-227-357-509
; Sequence 509, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 509
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-509

Query Match 11.4%; Score 136; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 VFSCIYGEGYSNAHESKQMYCVFN 62
||||||||||||||||||||||||
Db 1 VFSCIYGEGYSNAHESKQMYCVFN 24

RESULT 5
US-09-621-976-4130
; Sequence 4130, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4130
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1
US-09-621-976-4130

Query Match 11.2%; Score 133; DB 4; Length 56;
Best Local Similarity 49.0%; Pred. No. 1.1e-07;
Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNA 51
              || ||||| ||||:||    : ||  :  | |  :|:::||  |  ||| |:
Db          1 MEGGAYGAGKAGGAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNS 51
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RESULT 6
US-09-227-357-510
; Sequence 510, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 510
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-510

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  Query Match             7.8%;  Score 93;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 RNEDACRYGSAIGVLAFL 80
              ||||||||||||||||||
Db          1 RNEDACRYGSAIGVLAFL 18
```

RESULT 7
US-09-874-923-121
; Sequence 121, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Leishmania major and chagasi
US-09-874-923-121

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  Query Match             7.8%;  Score 93;  DB 4;  Length 709;
  Best Local Similarity   25.1%;  Pred. No. 0.14;
  Matches   47;  Conservative   21;  Mismatches   73;  Indels   46;  Gaps    8;

Qy         12 GGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGE-----------GYSNA-HESKQMYC 59
              |||           ||| ||||     : :|::                |:|:|  |    |
Db          6 GGSL---------AVVALAVCLAVLAAIGTCVFDSQEIGGSSFTFVGWSSASKEESYQGC 56

Qy         60 VF------------NRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNAT--DRKYLV 105
                          : ::||     |   :     :  |  |    ::|||  |||: :|  |   |    |
Db         57 TLTGKAFRIQGAASSLSDDATLPGGILRFSSLLVSNGYIVVDKYFPRNTNITIKDASGTV 116

Qy        106 IGDLLF----SALWTFLWFVGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGV 161
                : |      :|:::    :       |  ||          |   |||  |      |   |  |
Db        117 AAGMPFIDANTAIYSDQLSIVVTDSTLSWAAARS-----GQSMVRAPFTIQLSS--SLFV 169

Qy        162 LASLAYQ 168
              | |   |
Db        170 LGSTVTQ 176
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RESULT 8
US-09-227-357-511
; Sequence 511, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,954
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/058,785
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,664
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,660
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,661
;  EARLIER FILING DATE: 1997-09-12
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 511
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-227-357-511

  Query Match             7.2%;  Score 86;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.0037;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         86 LVVDAYFPQISNATDRK 102
              |||||||||||||||||
Db          1 LVVDAYFPQISNATDRK 17


RESULT 9
US-09-328-352-6877
; Sequence 6877, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6877
;   LENGTH: 442
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-6877

  Query Match             7.2%;  Score 86;  DB 4;  Length 442;
  Best Local Similarity   21.9%;  Pred. No. 0.42;
  Matches   42;  Conservative   31;  Mismatches   77;  Indels   42;  Gaps    7;

Qy         15 FDLRRFLTQ--PQVVARAVCL--VFALIVFSCIYGEGYSNAHESKQMYCVFNRNEDACRY 70
              | |: ||:   |: :| |:    :  ::||| :|   :  :: |:   | | |
Db        140 FTLQSFLSHVFPRSIAEAMANNDILQVLVFSIFFGSALAFVNQGKEKDSVIIRLTDE--- 196

Qy         71 GSAIGVLAFLASAFFLVVD--------AYFPQISNATDRKYL--------VIGDLLFS-- 112
                 |:   | : |         | |  |::|   : |         :| :  |
Db        197 ---------LSKIMFRITDYVMMFAPFAVFAAIASAITVQGLGLIVDYGILIAEFYFGLL 247

Qy        113 ALWTFLWFVGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKA 172
              ||  |: ||        |:   ||:      :|  :| :| :  |      :      |
Db        248 LLWVILFSVG--------AIVLKKDIFRLGKLIREPVTLAFATASSESAYPKVMDALNKF 299

Qy        173 GVDDFIQNYVDP 184
              ||   : ::| |
Db        300 GVPKKVTSFVLP 311


RESULT 10
US-09-107-532A-5264
; Sequence 5264, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
```

; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...155
; SEQUENCE DESCRIPTION: SEQ ID NO: 5264:
US-09-107-532A-5264

Query Match 7.1%; Score 85; DB 4; Length 155;
Best Local Similarity 26.6%; Pred. No. 0.12;
Matches 47; Conservative 27; Mismatches 67; Indels 36; Gaps 8;

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Qy          18 RRFLTQPQVVARAVCLV-----FALIVFSCIYGEGYS-NAHESKQMYCVFNRNEDACRYG 71
               :||::: : : :  ||:     | :|:|  : |||    ||                  |
Db           4 KRFVSKMKAIRKECCLMKFFQEFFIIIFFSVLGEGIRIFAHLPIP--------------G 49

Qy          72 SAIGVLAFLASAFFL-VVDAYFPQISNATDRKYLVIGDLLFSALWTFLWFVGFCFLTNQW 130
               | :|:| ||  || : :||   |:  ||       || | : |      |   |
Db          50 SILGIL-FLFLAFEMHLVD---PEKIGAT-------GDFLLNNLAILFVPAGVGLLEYFD 98

Qy         131 AVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYK----AGVDDFIQNYVD 183
                : :   ||:||  | : :|       : || | | | | |      |::  :| :|
Db          99 DIASIWPVLLGAVVVCSIVTMVAAGKTAEGVEALLGYVRKKKAERVSVNEMEENQID 155
```

RESULT 11
US-09-142-732-2
; Sequence 2, Application US/09142732
; Patent No. 6252045
; GENERAL INFORMATION:
; APPLICANT: James M. Anderson
; APPLICANT: Christina M. Van Itallie
; TITLE OF INVENTION: Human Occludin, Its Uses and
; TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yale University Medical School
; ADDRESSEE: Section of Digestive Diseases
; ADDRESSEE: Department of Internal Medicine
; STREET: 333 Cedar Street, LCI 105
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,732
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/05809
; FILING DATE: March 14, 1997
; APPLICATION NUMBER: U.S. 60/013,625
; FILING DATE: March 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 522
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; FRAGMENT TYPE: complete sequence
; FEATURE:
; NAME/KEY: human occludin
US-09-142-732-2

Query Match 7.1%; Score 85; DB 3; Length 522;
Best Local Similarity 16.2%; Pred. No. 0.7;
Matches 59; Conservative 46; Mismatches 92; Indels 168; Gaps 14;

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Qy          44 ------------------------YGEGYSNAHESKQMYCVFNRNEDACRYGSAIGVLAF 79
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Db          90 DRGYGTSLLGGSVGYPYGGSGFGSYGSGYGYGYGYGYGYGGYTDPRAAKGFMLAMAAFCF 149

Qy          80 LASAFFLVVDAYFPQISNATDRKYL-------VIGDLLFSALWTFLWFVG---------- 122
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Qy         185 TPDPNTAYAS---------YPGAS-----------------VDNYQQPPFTQ--NAETT 215
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Db         319 VDSP-MAYSSNGKVNDKRFYPESSYKSTPVPEVVQELPLTSPVDDFRQPRYSSGGNFETP 377

Qy         216 EGYQP 220
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Db         378 SKRAP 382
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RESULT 12
US-08-945-826-2
; Sequence 2, Application US/08945826
; Patent No. 6489460
; GENERAL INFORMATION:

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;    APPLICANT:  TSUKITA, Shoichiro
;    TITLE OF INVENTION:  HUMAN ADHESION MOLECULE OCCLUDIN
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch, LLP
;      STREET:  P.O. Box 747
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/945,826
;      FILING DATE:  05-NOV-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FARACI, C. Joseph
;      REGISTRATION NUMBER:  32,350
;      REFERENCE/DOCKET NUMBER:  0425-0660P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  522 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-945-826-2

  Query Match             7.1%;  Score 85;  DB 4;  Length 522;
  Best Local Similarity   16.2%;  Pred. No. 0.7;
  Matches   59;  Conservative   46;  Mismatches   92;  Indels  168;  Gaps   14;

Qy         12 GGSFDLRRFLTQPQV----------------------VARAVCLVFALIVFSCI------ 43
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Db         30 GGEMHVRPMLSQPAYSFYPEDEILHFYKWTSPPGVIRILSMLIIVMCIAIPACVASTLAW 89

Qy         44 ------------------------YGEGYSNAHESKQMYCVFNRNEDACRYGSAIGVLAF 79
                                      || ||   :    |  :     |  :  |:    |
Db         90 DRGYGTSLLGGSVGYPYGGSGFGSYGSGYGYGYGYGYGGYTDPRAAKGFMLAMAAFCF 149

Qy         80 LASAFFLVVDAYFPQISNATDRKYL-------VIGDLLFSALWTFLWFVG---------- 122
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Qy        123 -----FCFLTNQ----------------WAVTNPKDVLVGADSVRAAITFSFFSIFSWG 160
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Db        207 LYGSQIYALCNQFYTPAATGLYVDQYLYHYCVVDPQEAI--------AIVLGFMIIVAFA 258

Qy        161 VLASLA----------------------YQRYKAGVDDFIQN-------------YVDP 184
              ::   |                      |      |:::::|             ||:
Db        259 LIIFFAVKTRRKMDRYDKSNILWDKEHIYDEQPPNVEEWVKNVSAGTQDVPSPPSDYVER 318

Qy        185 TPDPNTAYAS---------YPGAS-----------------VDNYQQPPFTQ--NAETT 215
                | ||:|         || :|                  ||:::|| ::   | ||
Db        319 VDSP-MAYSSNGKVNDKRFYPESSYKSTPVPEVVQELPLTSPVDDFRQPRYSSGGNFETP 377

Qy        216 EGYQP 220
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Db        378 SKRAP 382


RESULT 13
US-09-197-503-2
; Sequence 2, Application US/09197503
; Patent No. 6559286
;  GENERAL INFORMATION:
;    APPLICANT:  TSUKITA, Shoichiro
;    TITLE OF INVENTION:  HUMAN ADHESION MOLECULE OCCLUDIN
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch, LLP
;      STREET:  P.O. Box 747
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/197,503
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/945,826
;      FILING DATE:  05-NOV-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FARACI, C. Joseph
;      REGISTRATION NUMBER:  32,350
;      REFERENCE/DOCKET NUMBER:  0425-0660P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  522 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-197-503-2

  Query Match             7.1%;  Score 85;  DB 4;  Length 522;
  Best Local Similarity   16.2%;  Pred. No. 0.7;
  Matches   59;  Conservative   46;  Mismatches   92;  Indels  168;  Gaps   14;

Qy         12 GGSFDLRRFLTQPQV----------------------VARAVCLVFALIVFSCI------ 43
              ||    :|  |:||                      :   : :|  : :|:|:
Db         30 GGEMHVRPMLSQPAYSFYPEDEILHFYKWTSPPGVIRILSMLIIVMCIAIFACVASTLAW 89

Qy         44 ------------------------YGEGYSNAHESKQMYCVFNRNEDACRYGSAIGVLAF 79
                                      || ||   :    |  :     |  :  |:    |
Db         90 DRGYGTSLLGGSVGYPYGGSGFGSYGSGYGYGYGYGYGGYTDPRAAKGFMLAMAAFCF 149

Qy         80 LASAFFLVVDAYFPQISNATDRKYL-------VIGDLLFSALWTFLWFVG---------- 122
              :|:    |       ::|  | | ||       ::| ::|  |  | :: :|
Db        150 IAALVIFVTSVIRSEMSR-TRRYYLSVIIVSAILGIMVFIA--TIVYIMGVNPTAQSSGS 206

Qy        123 -----FCFLTNQ----------------WAVTNPKDVLVGADSVRAAITFSFFSIFSWG 160
                  | ||                : | :|:: :        ||   |  | ::
Db        207 LYGSQIYALCNQFYTPAATGLYVDQYLYHYCVVDPQEAI--------AIVLGFMIIVAFA 258

Qy        161 VLASLA----------------------YQRYKAGVDDFIQN-------------YVDP 184
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Db        259 LIIFFAVKTRRKMDRYDKSNILWDKEHIYDEQPPNVEEWVKNVSAGTQDVPSPPSDYVER 318

Qy        185 TPDPNTAYAS---------YPGAS-----------------VDNYQQPPFTQ--NAETT 215
                | ||:|         || :|                  ||:::|| ::   | ||
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Qy        216 EGYQP 220
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Db        378 SKRAP 382


RESULT 14
US-08-933-750C-30
; Sequence 30, Application US/08933750C
; Patent No. 5932442
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;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  HUMAN REGULATORY MOLECULES
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/933,750C
;      FILING DATE:  September 23, 1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0356 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BLADNOT03
;      CLONE:  1600438
US-08-933-750C-30

  Query Match             7.1%;  Score 84;  DB 2;  Length 419;
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  Matches   43;  Conservative   38;  Mismatches   99;  Indels   44;  Gaps    5;

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Qy         58 -YCVFNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWT 116
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RESULT 15
US-09-234-613-30
; Sequence 30, Application US/09234613
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; Patent No. 6132973
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  HUMAN REGULATORY MOLECULES
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,613
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/933,750
;      FILING DATE:  September 23, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0356 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BLADNOT03
;      CLONE:  1600438
US-09-234-613-30

  Query Match             7.1%;  Score 84;  DB 3;  Length 419;
  Best Local Similarity   19.2%;  Pred. No. 0.66;
  Matches   43;  Conservative   38;  Mismatches   99;  Indels   44;  Gaps    5;

Qy          1 MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQM--- 57
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Db         45 LEAVAKFLDSTGSRLDYRRYAD----------TLFDILVAGSMLAPGGTRIDDGDKTKMT 94

Qy         58 -YCVFNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWT 116
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Qy        117 FLWFVGFCFLTNQWAVTNPKDVLVGADSVRAAITFSFF--SIFSWGVLASLAYQRYKAGV 174
               | |:     | |  :     :|:|  :: | |  | |  |:  |: || | : :|| :
Db        136 LLLFLKAFSETEQTKLAMLSGILLGNGTLPATILTSLFTDSLVKEGIAASFAVKLFKAWM 195

Qy        175 DDFIQNYVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGY 218
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GenCore version 5.1.6

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 10

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	732	48.4	969	2	US-08-700-637-1	Sequence 1, Appli
	2	633	41.9	1977	4	US-09-227-357-83	Sequence 83, Appl
	3	337	22.3	396	4	US-09-640-173-135	Sequence 135, App
	4	337	22.3	396	4	US-09-713-550-135	Sequence 135, App
	5	176	11.6	232	2	US-08-700-637-5	Sequence 5, Appli
	6	159	10.5	230	2	US-08-700-637-10	Sequence 10, Appl
	7	143	9.5	265	2	US-08-700-637-7	Sequence 7, Appli
	8	129	8.5	296	2	US-08-700-637-11	Sequence 11, Appl
	9	121	8.0	272	2	US-08-700-637-6	Sequence 6, Appli
	10	93	6.2	339	2	US-08-700-637-12	Sequence 12, Appl
	11	80	5.3	115	4	US-09-621-976-18432	Sequence 18432, A
	12	80	5.3	134	4	US-09-621-976-18433	Sequence 18433, A
	13	80	5.3	137	4	US-09-621-976-18434	Sequence 18434, A
	14	73	4.8	192	2	US-08-700-637-8	Sequence 8, Appli
	15	51	3.4	51	4	US-09-443-199C-751	Sequence 751, App
	16	32	2.1	220	2	US-08-700-637-9	Sequence 9, Appli
	17	25	1.7	51	4	US-09-443-199C-752	Sequence 752, App
	18	25	1.7	493	4	US-09-280-116-166	Sequence 166, App
	19	25	1.7	493	4	US-09-392-184-20	Sequence 20, Appl
	20	25	1.7	508	4	US-09-280-116-47	Sequence 47, Appl
	21	25	1.7	601	4	US-09-336-536-74	Sequence 74, Appl
	22	25	1.7	4333	4	US-09-833-381-885	Sequence 885, App
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	25	24	1.6	351	4	US-09-280-116-45	Sequence 45, Appl
c	26	24	1.6	412	4	US-09-764-325A-17	Sequence 17, Appl
c	27	24	1.6	412	4	US-09-912-935-17	Sequence 17, Appl
	28	24	1.6	465	4	US-09-833-381-1892	Sequence 1892, Ap
c	29	24	1.6	494	4	US-09-833-381-1944	Sequence 1944, Ap
c	30	24	1.6	496	4	US-09-573-906-8	Sequence 8, Appli
c	31	24	1.6	511	4	US-09-976-594-110	Sequence 110, App
c	32	24	1.6	546	4	US-09-280-116-48	Sequence 48, Appl
	33	24	1.6	591	4	US-09-833-381-1165	Sequence 1165, Ap
c	34	24	1.6	618	4	US-09-833-381-1049	Sequence 1049, Ap
c	35	24	1.6	640	4	US-09-569-804-18	Sequence 18, Appl
c	36	24	1.6	749	4	US-09-257-583-12	Sequence 12, Appl
	37	24	1.6	792	3	US-08-950-720A-1	Sequence 1, Appli
c	38	24	1.6	810	4	US-09-072-993C-5	Sequence 5, Appli
c	39	24	1.6	823	4	US-09-227-357-78	Sequence 78, Appl
c	40	24	1.6	860	4	US-09-833-381-1390	Sequence 1390, Ap
c	41	24	1.6	908	4	US-09-800-729-25	Sequence 25, Appl
c	42	24	1.6	944	4	US-09-227-357-122	Sequence 122, App
	43	24	1.6	1021	4	US-09-280-116-85	Sequence 85, Appl
c	44	24	1.6	1022	4	US-09-489-847-75	Sequence 75, Appl
c	45	24	1.6	1041	4	US-09-690-454-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-700-637-1
; Sequence 1, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT05
; CLONE: 775426
US-08-700-637-1

Query Match 48.4%; Score 732; DB 2; Length 969;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 26 CGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGG 85

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Db         85 CGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGGGCCTACGGCGCGGCCAAGGCGGG 144

Qy         86 CGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTG 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTG 204

Qy        146 CTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCA 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 CTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCA 264

Qy        206 CGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAG 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAG 324

Qy        266 TGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTT 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATTT 384

Qy        326 CCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTC 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTC 444

Qy        386 AGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGT 445
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGCTCTCTGGACCTTGCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGT 504

Qy        446 CACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAG 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 CACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCATCACCTTCAG 564

Qy        506 CTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGC 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCTACAAGGC 624

Qy        566 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTGCCTA 684

Qy        626 CGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGC 744

Qy        686 GGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAAG 745
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        745 GGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGTTAGCGTGGGAAG 804

Qy        746 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCC 805
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        805 GGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCTCCTGGAACTGCC 864

Qy        806 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATA 924

Qy        866 GCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCA 910
              |||||||||||||||||||||||||||||||||||||||||||||
Db        925 GCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCA 969


RESULT 2
US-09-227-357-83
; Sequence 83, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,954
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/058,785
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,664
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,660
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,661
;  EARLIER FILING DATE: 1997-09-12
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
;  LENGTH: 1977
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (664)
;  OTHER INFORMATION: n equals a,t,g, or c
;  FEATURE:
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;   NAME/KEY: SITE
;   LOCATION: (716)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1319)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-83

  Query Match             41.9%;  Score 633;  DB 4;  Length 1977;
  Best Local Similarity   99.5%;  Pred. No. 8.7e-296;
  Matches  953;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       554 GCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCC 613
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       957 GCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCC 1016

Qy       614 CAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTT 673
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1017 CAACACTGCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTT 1076

Qy       674 CACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGT 733
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db      1077 CACCCAGAACGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGCGGCGGT 1136

Qy       734 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCT 793
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db      1137 TAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATGAGCCT 1196

Qy       794 CCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTA 853
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1197 CCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTA 1256

Qy       854 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 913
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1257 AGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAG 1316

Qy       914 GGCTTCAGTCAGCCGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 973
            || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1317 GGNTTCAGTCAGCYGCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGT 1376

Qy       974 TTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCC 1033
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1377 TTTTCCTCGCTTTTAATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCC 1436

Qy      1034 ATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCT 1093
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1437 ATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCT 1496

Qy      1094 ATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGA 1153
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1497 ATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGA 1556

Qy      1154 GCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATG 1213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1557 GCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATG 1616

Qy      1214 ATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCG 1273
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1617 ATCTGGGGGCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCG 1676

Qy      1274 GGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTG 1333
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      1677 GGGCTGGTGCTCATGGCACTTCCTCCTTGCTCCCACCCCTGGCAGCAGGGAA-GGCTTTG 1735

Qy      1334 CCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAG 1393
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1736 CCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTTGTTACTTAGGAAGCCTGGGGAG 1795

Qy      1394 GGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGG 1453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1796 GGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAAATCGTGG 1855

Qy      1454 GGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTCATTCAAA 1511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1856 GGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTCATTCAAA 1913


RESULT 3
US-09-640-173-135
; Sequence 135, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION:  OVARIAN TUMOR SEQUENCES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE:  210121.4B4C2
;  CURRENT APPLICATION NUMBER: US/09/640,173
;  CURRENT FILING DATE:  2000-08-15
;  NUMBER OF SEQ ID NOS:  196
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 135
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-640-173-135

  Query Match             22.3%;  Score 337;  DB 4;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-153;
  Matches  337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       928 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTT 987
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        60 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTT 119

Qy       988 AATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACA 1047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       120 AATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACA 179

Qy      1048 AGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCT 1107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       180 AGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCT 239

Qy      1108 CTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTC 1167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       240 CTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTC 299

Qy      1168 TTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACC 1227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       300 TTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACC 359

Qy      1228 ACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGT 1264
            ||||||||||||||||||||||||||||||||||||
Db       360 ACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGT 396


RESULT 4
US-09-713-550-135
; Sequence 135, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE:  210121.484C4
;  CURRENT APPLICATION NUMBER: US/09/713,550
;  CURRENT FILING DATE:  2000-11-14
;  NUMBER OF SEQ ID NOS:  205
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 135
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-713-550-135
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  Query Match             22.3%;  Score 337;  DB 4;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-153;
  Matches  337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        928 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTT 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 GCTCACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTT 119

Qy        988 AATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACA 1047
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 AATGACCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACA 179

Qy       1048 AGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCT 1107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AGTGCCTCAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCT 239

Qy       1108 CTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTC 1167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTC 299

Qy       1168 TTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACC 1227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACC 359

Qy       1228 ACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGT 1264
              |||||||||||||||||||||||||||||||||||||
Db        360 ACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGT 396
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RESULT 5
US-08-700-637-5
; Sequence 5, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: TMLR2DT01
; CLONE: 392250
US-08-700-637-5

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  Query Match             11.6%;  Score 176;  DB 2;  Length 232;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-75;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         72 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTG 60

Qy        132 GCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 191
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 GCGCGCGCCGTGTGCTTGGTCTTCGNCTTGATCGTGTTCTCCTGCATCTATGGTGAGGGC 120

Qy        192 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCC 180

Qy        252 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGC 298
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGC 227
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RESULT 6
US-08-700-637-10
; Sequence 10, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT02
; CLONE: 754306
US-08-700-637-10

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  Query Match             10.5%;  Score 159;  DB 2;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-67;
  Matches  159;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        126 GTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGT 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 GTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGT 131
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Qy        186 GAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAG 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAG 191

Qy        246 GATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCC 284
              |||||||||||||||||||||||||||||||||||||||
Db        192 GATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCC 230


RESULT 7
US-08-700-637-7
; Sequence 7, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  COLNNOT01
;      CLONE:  608493
US-08-700-637-7

  Query Match             9.5%;  Score 143;  DB 2;  Length 265;
  Best Local Similarity   99.2%;  Pred. No. 2.7e-59;
  Matches  243;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         57 AGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACG 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACG 60

Qy        117 CAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGC 176
              |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
Db         61 CAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTNGTCTTCGCCTTGATCGTNTTCTCCTGC 120

Qy        177 ATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAAC 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAAC 180

Qy        237 CGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCG 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCG 240

Qy        297 GCCTT 301
              |||||
Db        241 GCCTT 245


RESULT 8
US-08-700-637-11
; Sequence 11, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  296 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGNOT04
;      CLONE:  809604
US-08-700-637-11

  Query Match             8.5%;  Score 129;  DB 2;  Length 296;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-52;
  Matches  129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCA 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCA 189

Qy        218 GATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGT 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GATGTACTGCGTGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGT 249

Qy        278 GCTGGCCTT 286
              |||||||||
Db        250 GCTGGCCTT 258


RESULT 9
US-08-700-637-6
; Sequence 6, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
```

```
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  MMLR2DT01
;      CLONE:  476266
US-08-700-637-6

  Query Match             8.0%;  Score 121;  DB 2;  Length 272;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 AGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCA 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 AGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCA 142

Qy        178 TCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 TCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACC 202

Qy        238 G 238
              |
Db        203 G 203


RESULT 10
US-08-700-637-12
; Sequence 12, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGAST01
;      CLONE:  868416
US-08-700-637-12

  Query Match             6.2%;  Score 93;  DB 2;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-35;
  Matches   93;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCA 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CTTGATCGTGTTCTCCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCA 171

Qy        218 GATGTACTGCGTGTTCAACCGCAACGAGGATGC 250
              ||||||||||||||||||||||||||||||||
Db        172 GATGTACTGCGTGTTCAACCGCAACGAGGATGC 204


RESULT 11
US-09-621-976-18432
; Sequence 18432, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 18432
;   LENGTH: 115
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-18432

  Query Match             5.3%;  Score 80;  DB 4;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-29;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 1491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 60

Qy       1492 TAAATGTTTTCTCATTCAAA 1511
              ||||||||||||||||||||
Db         61 TAAATGTTTTCTCATTCAAA 80


RESULT 12
```

```
US-09-621-976-18433
; Sequence 18433, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 18433
;   LENGTH: 134
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-18433

  Query Match             5.3%;  Score 80;  DB 4;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-29;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 1491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 60

Qy       1492 TAAATGTTTTCTCATTCAAA 1511
             ||||||||||||||||||||
Db         61 TAAATGTTTTCTCATTCAAA 80


RESULT 13
US-09-621-976-18434
; Sequence 18434, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 18434
;   LENGTH: 137
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-18434

  Query Match             5.3%;  Score 80;  DB 4;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-29;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 1491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAA 60

Qy       1492 TAAATGTTTTCTCATTCAAA 1511
             ||||||||||||||||||||
Db         61 TAAATGTTTTCTCATTCAAA 80


RESULT 14
US-08-700-637-8
; Sequence 8, Application US/08700637
; Patent No. 5854413
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,637
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0065 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGTUT02
;      CLONE:  693335
US-08-700-637-8

  Query Match             4.8%;  Score 73;  DB 2;  Length 192;
  Best Local Similarity   99.2%;  Pred. No. 1.7e-25;
  Matches  123;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        126 GTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         56 GTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATNTATGGT 115

Qy        186 GAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAG 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 GAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAG 175

Qy        246 GATG 249
              ||||
Db        176 GATG 179


RESULT 15
US-09-443-199C-751
; Sequence 751, Application US/09443199C
; Patent No. 6670464
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  Leach, Martin
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms and Methods of Use Thereof
;  FILE REFERENCE: 15966-534A
;  CURRENT APPLICATION NUMBER: US/09/443,199C
;  CURRENT FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER: 60/109,024
;  PRIOR FILING DATE: 1998-11-17
;  NUMBER OF SEQ ID NOS: 1272
;  SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 751
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (752 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg43921107
US-09-443-199C-751

  Query Match              3.4%;  Score 51;  DB 4;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-15;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        274 GGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATT 324
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGTATT 51


Search completed: April  8, 2004, 13:45:49
Job time : 139 secs
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